OIPE JC141
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1
A

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2                                                  32
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62                                                 92
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122                                                152
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182                                                212
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242                                                272
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302                                                332
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362                                                392
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422                                                452
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482                                                512
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542                                                572
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602                                                632
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662                                                692
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met
```

FIG. 1

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722                                                 752
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782                                                 812
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842              |Cadherin Cleavage|          872
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902                                                 932
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962                                                 992
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly

1022                                               1052
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082                                               1112
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142                                               1172
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202                                               1232                    |Cadherin EC
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

xxx|                                               1292
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu

1322                                               1352
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382                                              1412/471
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442                                               1472
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser
```

FIG. 1 (cont.)

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1502                                                1532
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn

1562                                                1592
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622                                                1652
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp

1682                                                1712
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742                                                1772
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802                                                1832
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862                                                1892
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val

1922                                                1952
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982                                                2012
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042                                                2072
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102                                                2132
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

2162                                                2192
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

2222                                                2252
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu
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FIG. 1 (cont.)

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2282                                                2312
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342                                                2372
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402                                                2432
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462                                                2492
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522                                                2552
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582                                                2612
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642                                                2672
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702                                                2732
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762                                                2792
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822                                        2852    |xxxxxxxxxxxxxxxx Predicted
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

Transmembrane Domain xxxxxxxxxxxxxxxxxxxxxxxxxxxx|
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942                                                2972
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu

3002                                                3032
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062                                                3092
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT
cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu
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FIG. 1 (cont.)

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3122                                                3155
ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT
ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182                                                3212
ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG
ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu

3242                                                3272
TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC
tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302                                                3332
CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT
pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362                                                3392
GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC
asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422                                                3452
TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG
phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln

3482                                                3512
TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC
cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys lys arg ile

3542                                                3572    |xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG
pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

3602 xxx  Coiled-Coil 1  xxxxxxxxxxxxxx  3632 xxxx  Coiled-Coil 1  xxxxxxxxxxxxxx
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA
ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys

3662 xxxxxxxxxxxxxxxxxxxxxxxx|                    3692
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722                                                3752
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782                                                3812                    |xxxxxxxxxxxxxxxxxx
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu
```

FIG. 1 (cont.)

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3842 xxx  Coiled-Coil 2  xxxxxxxxxxxxx  3872 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

3902 xxx  Coiled-Coil 2  xxxxxxxxxxxxx  3932 xxxxx|
ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962                                                3992
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022                                    |xxxx PBM xxxx|
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG
met val his gly met thr ser ser ser ser val val STP

4082                                                4112
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142                                                4172
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202                                                4232
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262                                                4292
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322                                                4352
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382                                                4412
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

4442                                                4472
CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502                                                4532
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562                                                4592
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622                                                4652
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682                                                4712
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742                                                4772
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802
TTT ACT
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FIG. 1 (cont.)

(Nucleotide position for insertions and deletions are found above the Human (h) CLASP-2A line diagram. Numbers are referenced based on hCLASP-2A nucleotide sequence from Figure 1.)

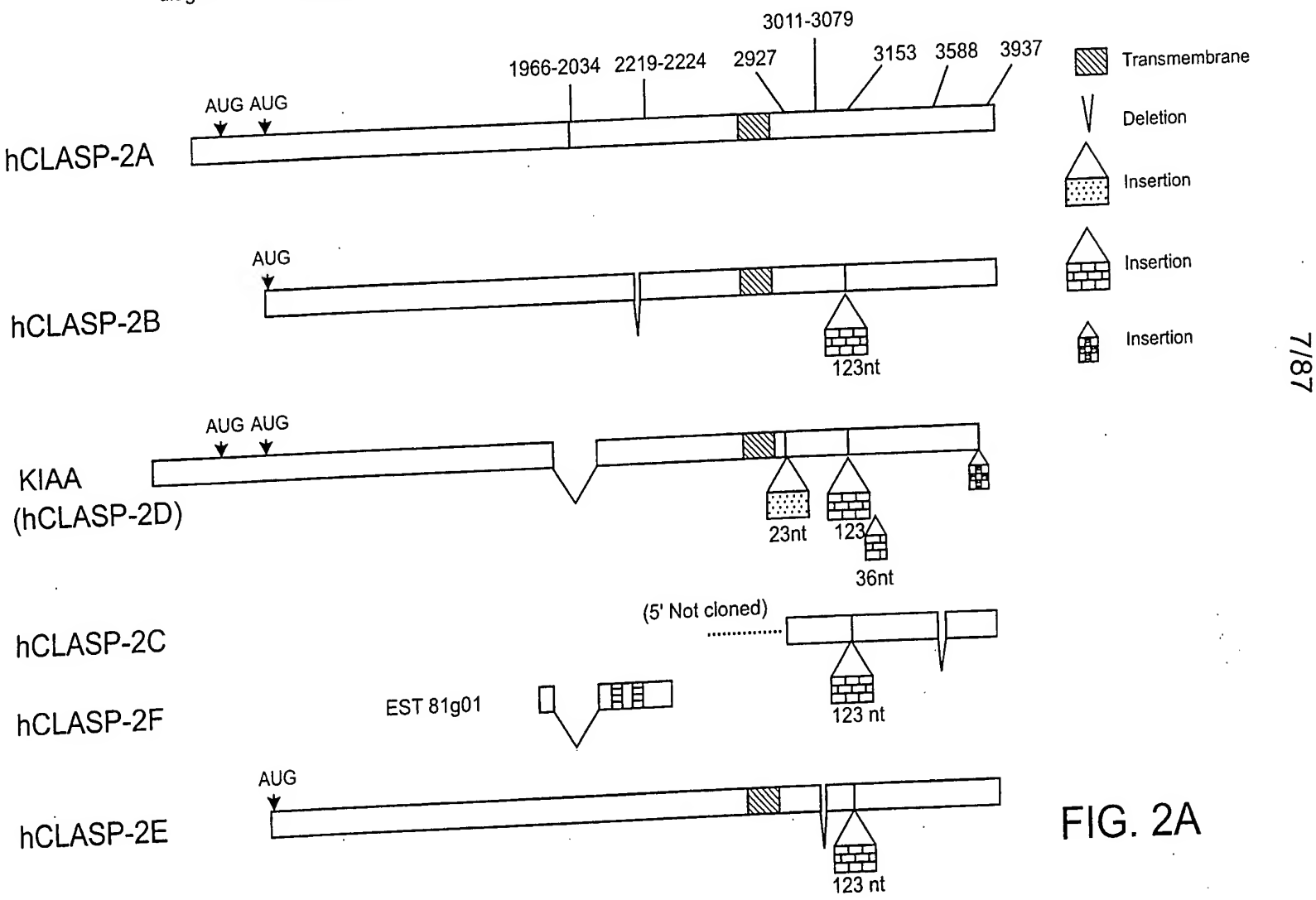

FIG. 2A

1
A

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2                                                32
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62                                               92
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122                                              152
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182                                              212
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242                                              272
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302                                              332
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362                                              392
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422                                              452
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482                                              512
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542                                              572
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602                                              632
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662                                              692
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met
```

FIG. 2B

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722                                                 752
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782                                                 812
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842              |Cadherin Cleavage|      872
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902                                                 932
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962                                                 992
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly

1022                                               1052
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082                                               1112
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142                                               1172
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202                                               1232                    |Cadherin EC
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

xxx|                                               1292
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu

1322                                               1352
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382                                               1412
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442                                               1472
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser
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FIG. 2B (cont.)

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1502                                                1532
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn

1562                                                1592
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622                                                1652
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp

1682                                                1712
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742                                                1772
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802                                                1832
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862                                                1892
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val

1922                                                1952                |xxxxxxxxxxxxxxxxxxxxx
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982 xxxxxxxxxx  deleted in CLASP-2D(KIAA1058) xxxxxxxxxxxxxxxxxxxxxxx|
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042                                                2072
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102                                                2132
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

                                                                                Deleted
                                                                                |xxx
2162                                                2192
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

in HC2B
xxx|                                                2252
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu
```

FIG. 2B (cont.)

```
2282                                                2312
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342                                                2372
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402                                                2432
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462                                                2492
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522                                                2552
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582                                                2612
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642                                                2672
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702                                                2732
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762                                                2792
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822                                        2852    |xxxxxxxxxxxxxxx Predicted
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

    [Additional and differential exon usage found at position 2927 consisting
    of 69 nucleotides.  This entire sequence is found in Human CLASP-2D
    (KIAA1058) and not other isoforms of CLASP-2. It has a sequence of:
    AAGCAGTCCAGTGGGAGCCGCCCCTTCTCCCCCACAGCCATAGCGCCTGCCTGAGGAGGAGCCGGGGAG]

Transmembrane Domain xxxxxxxxxxxxxxxxxxxxxxxxxxxx|
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942                                                2972
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu
```

FIG. 2B (cont.)

3002 |xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Sequence deleted in CLASP-2E xxxxx
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062 xxxxxxxxxxxxxxxxxx| 3092
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT
cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

[Additional and differential exon usage found at position 3153. The entire sequence below is found in Human CLASP-2D. Underlined sequence is found in Human CLASP-2B, 2C and 2E.
TGAGAGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCAT
GCACTCGGGCCGCAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGGCAGCGCAATACCAGTTT
ACAGACAGTGAAACAGATGTGGAGGGATT]

3122 3155
ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT
ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182 3212
ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG
ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu

3242 3272
TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC
tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302 3332
CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT
pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362 3392
GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC
asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422 3452
TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG
phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln

3482 3512
TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC
cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys lys arg ile

Two nucleotide deletion (nts 3586 and 3587) found in Human CLASP-2C

3542 3572 |xxx|
CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG
pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

FIG. 2B (cont.)

```
3602                                                3632
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA
ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys

3662                                                3692
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722                                                3752
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782                                                3812
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

3842                                                3872
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu


Insertion of 8 nucleotides found only in Human CLASP-2D with sequence: CTGGGATG

3902                                                3932
ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962                                                3992
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022                                    |xxxx PBM xxxx|
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG
met val his gly met thr ser ser ser ser val val STP

4082                                                4112
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142                                                4172
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202                                                4232
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262                                                4292
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322                                                4352
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382                                                4412
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG
```

FIG. 2B (cont.)

```
4442                                                4472
CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502                                                4532
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562                                                4592
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622                                                4652
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682                                                4712
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742                                                4772
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802
TTT ACT
```

FIG. 2B (cont.)

```
HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GCATCTGGAAATCTTGACAAAAATGCCAGATTTTCTGCCATCTACAGGCAAGACAGCAAT
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   AAGCTATCCAATGATGACATGCTCAAGTTACTTGCAGACTTTCGGAAACCTGAGAAGATG
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GCTAAGCTCCCAGTGATTTTAGGCAATCTAGACATTACAATTGATAATGTTTCCTCAGAC
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TTCCCTAATTATGTTAATTCATCATACATTCCCACAAAACAATTTGAAACCTGCAGTAAA
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   ACTCCCATCACGTTTGAAGTGGAGGAATTTGTGCCCTGCATACCAAAACACACTCAGCCT
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------
```

FIG. 3A

```
HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TACACCATCTACACCAATCACCTTTACGTTTATCCTAAGTACTTGAAATACGACAGTCAG
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   AAGTCTTTTGCCAAGGCTAGAAATATTGCGATTTGCATTGAATTCAAAGATTCAGATGAG
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GAAGACTCTCAGCCCCTTAAGTGCATTTATGGCAGACCTGGTGGGCCAGTTTTCACAAGA
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            --------------AGTTTTACACCATCACCAAAACCCAGAATTTTATGATGAGATTAAA
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   AGCGCCTTTGCTGCAGTTTTACACCATCACCAAAACCCAGAATTTTATGATGAGATTAAA
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ATAGAGTTGCCCACTCAGCTGCATGAAAAGCACCACCTGTTGCTCACATTCTTCCATGTC
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   ATAGAGTTGCCCACTCAGCTGCATGAAAAGCACCACCTGTTGCTCACATTCTTCCATGTC
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            AGCTGTGACAACTCAAGTAAAGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTT
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   AGCTGTGACAACTCAAGTAAAGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTT
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            GGCTACTCCTGGCTTCCCCTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATC
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GGCTACTCCTGGCTTCCCCTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATC
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            CCGGTCTCGGCGAACCTTCCTTCGGGCTATCTTGGCTACCAAGAGCTTGGGATGGGCAGG
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CCGGTCTCGGCGAACCTTCCTTCGGGCTATCTTGGCTACCAGGAGCTTGGGATGGGCAGG
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            CATTATGGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACT
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CATTATGGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACT
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            CATCTGGTTTCTACAGTGTATACTCAGGATCAGCATTTACATAATTTTTTCCAGTACTGT
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CATCTGGTTTCTACAGTGTATACTCAGGATCAGCATTTACATAATTTTTTCCAGTACTGT
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            CAGAAAACCGAATCTGGAGCCCAAGCCTTAGGAAACGAACTTGTAAAGTACCTTAAGAGT
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CAGAAAACCGAATCTGGAGCCCAAGCCTTAGGAAACGAACTTGTAAAGTACCTTAAGAGT
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            CTGCATGCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2-80          ------------------------------------------------------------
HC2B            ------GCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CTGCATGCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2E            ------GCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2F            ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2-80          ------------------------------------------------------------
HC2B            TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2E            TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2F            ------------------------------------------------------------

HC2A            ATTCATGTGGTTGCCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2-80          ------------------------------------------------------------
HC2B            ATTCATGTGGTTGCCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   ATTCATGTGGTTGCCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2E            ATTCATGTGGTTGCCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2F            ------------------------------------------------------------

HC2A            AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2-80          ------------------------------------------------------------
HC2B            AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2E            AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2F            ------------------------------------------------------------

HC2A            CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCCTCACCAGCAACAAA
HC2-80          ------------------------------------------------------------
HC2B            CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCCTCACCAGCAACAAA
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCCTCACCAGCAACAAA
HC2E            CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCCTCACCAGCAACAAA
HC2F            ------------------------------------------------------------

HC2A            CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2-80          ------------------------------------------------------------
HC2B            CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CTACTGAAGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2E            CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2F            ------------------------------------------------------------

HC2A            ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCTGCATCCTATCATCAT
HC2-80          ------------------------------------------------------------
HC2B            ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCTGCATCCTATCATCAT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCTGCATCCTATCATCAT
HC2E            ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCTGCATCCTATCATCAT
HC2F            ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2-80          ------------------------------------------------------------
HC2B            GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GCAGTGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTCGAGATAAT
HC2E            GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2F            ------------------------------------------------------------

HC2A            CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2-80          ------------------------------------------------------------
HC2B            CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2E            CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2F            ------------------------------------------------------------

HC2A            TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACTACATTAGCTGTTTTGCTCCT
HC2-80          ------------------------------------------------------------
HC2B            TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACTACATTAGCTGTTTTGCTCCT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACTACATTAGCTGTTTTGCTCCT
HC2E            TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACTACATTAGCTGTTTTGCTCCT
HC2F            ------------------------------------------------------------

HC2A            GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2-80          ------------------------------------------------------------
HC2B            GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2E            GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2F            ------------------------------------------------------------

HC2A            GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2-80          ------------------------------------------------------------
HC2B            GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2E            GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2F            ------------------------------------------------------------

HC2A            CAAGACCTCCAGCTTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2-80          -------TCCAGCTTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2B            CAAGACCTCCAGCTTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CAAGACCTCCAGCTTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2E            CAAGACCTCCAGCTTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2F            ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2-80          GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2B            GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2E            GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2F            ------------------------------------------------------------

HC2A            GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2-80          GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2B            GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2E            GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2F            ------------------------------------------------------------

HC2A            AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2-80          AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2B            AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2E            AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2F            ------------------------------------------------------------

HC2A            AACGTCCAGCGGATCAATGTGAGGGATGTGTCACCCTTCCCTGTGAACGCGGGCATGACC
HC2-80          AACGTCCAGCGGATCAATGTGAGGGATGTGTCACCCTTCCCTGTGAACGCGGGCATGACC
HC2B            AACGTCCAGCGGATCAATGTGAGGGATGTGTCACCCTTCCCTGTGAACGCGGGCATGACC
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   AACGTCCAGCGGATCAATGTGAGGGATGTGTCACCCTTCCCTGTGAACGCGGGCATGACT
HC2E            AACGTCCAGCGGATCAATGTGAGGGATGTGTCACCCTTCCCTGTGAACGCGGGCATGACC
HC2F            ------------------------------------------------------------

HC2A            GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2-80          GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2B            GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2E            GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2F            ------------------------------------------------------------

HC2A            AGCACCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2-80          AGCACCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2B            AGCACCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   AGCACCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2E            AGCACCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2F            ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTCGAGAGGATCT
HC2-80          CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTCGAGAGGATCT
HC2B            CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTCGAGAGGATCT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTCGAGAGGATCT
HC2E            CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTCGAGAGGATCT
HC2F            ----------------------------------------GCTGATTCGAGAGGATCT

HC2A            CTCATAAGCACAGATTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2-80          CTCATAAGCACAGATTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2B            CTCATAAGCACAGATTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CTCATAAGCACAGATTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2E            CTCATAAGCACAGATTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2F            CTCATAAGCACAGATTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC

HC2A            CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2-80          CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2B            CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2E            CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2F            CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT

HC2A            GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT
HC2-80          GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT
HC2B            GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT
HC2E            GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT
HC2F            GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT

HC2A            GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACTTATGGATTTTTTT
HC2-80          GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACTTATGGATTTTTTT
HC2B            GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACTTATGGATTTTTTT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACTTATGGATTTTTTT
HC2E            GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACTTATGGATTTTTTT
HC2F            GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACTTATGGATTTTTTT

HC2A            ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2-80          ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2B            ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAG-
HC2E            ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2F            ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAG-
```

FIG. 3A (cont.)

```
HC2A            AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2-80          AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2B            AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   ----------------------------------AA----------------------
HC2E            AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2F            ----------TGTGA----------------GAAAG------ATATCAAGTGT----

HC2A            CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2-80          CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2B            CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   ----------CAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2E            CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2F            ------------------------------------GCTTGGAA--------------

HC2A            CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2-80          CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2B            CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2E            CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2F            -TTTCTGTAGACAATGGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT

HC2A            GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA
HC2-80          GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA
HC2B            GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA
HC2E            GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA
HC2F            GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA

HC2A            TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2-80          TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2B            TTGGCGTTTAAG------CTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2E            TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2F            TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAAAA

HC2A            TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2-80          TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2B            TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2E            TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2F            A-----------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A              TTCACTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2-80            TTCACTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2B              TTCACTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     TTCACTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2E              TTCACTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2F              ------------------------------------------------------------

HC2A              GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACTCCAAGCTGAGCTCC
HC2-80            GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACTCCAAGCTGAGCTCC
HC2B              GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACTCCAAGCTGAGCTCC
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACTCCAAGCTGAGCTCC
HC2E              GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACTCCAAGCTGAGCTCC
HC2F              ------------------------------------------------------------

HC2A              ATCAGGACGGAGGCCTCCCAGCTGCTCTACTTCCTGATGAGGAACAACTTTGATTACACT
HC2-80            ATCAGGACGGAGGCCTCCCAGCTGCTCTACTTCCTGATGAGGAACAACTTTGATTACACT
HC2B              ATCAGGACGGAGGCCTCCCAGCTGCTCTACTTCCTGATGAGGAACAACTTTGATTACACT
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     ATCAGGACGGAGGCCTCCCAGCTGCTCTACTTCCTGATGAGGAACAACTTTGATTACACT
HC2E              ATCAGGACGGAGGCCTCCCAGCTGCTCTACTTCCTGATGAGGAACAACTTTGATTACACT
HC2F              ------------------------------------------------------------

HC2A              GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTCAGCCAGCTGATA
HC2-80            GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTCAGCCAGCTGATA
HC2B              GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTCAGCCAGCTGATA
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTCAGCCAGCTGATA
HC2E              GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTCAGCCAGCTGATA
HC2F              ------------------------------------------------------------

HC2A              GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2-80            GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2B              GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     GCAGACGTTGTTGGCATTGGGGGAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2E              GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2F              ------------------------------------------------------------

HC2A              TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2-80            TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2B              TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2E              TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2F              ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2-80          ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2B            ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2E            ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2F            ------------------------------------------------------------

HC2A            CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCGAG
HC2-80          CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCGAG
HC2B            CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCGAG
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCGAG
HC2E            CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCGAG
HC2F            ------------------------------------------------------------

HC2A            CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2-80          CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2B            CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2E            CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2F            ------------------------------------------------------------

HC2A            GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2-80          GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2B            GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2E            GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2F            ------------------------------------------------------------

HC2A            G-----------------------------------------------------------
HC2-80          G-----------------------------------------------------------
HC2B            G-----------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GAAGCAGTCCAGTGGGAGCCGCCCCTTCTCCCCCACAGCCATAGCGCCTGCCTGAGGAGG
HC2E            G-----------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ----------GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2-80          ----------GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2B            ----------GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2C            ----------GTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2D-KIAA1058   AGCCGGGGAGGCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2E            ----------GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2F            ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
HC2-80          GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
HC2B            GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
HC2C            GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
HC2D-KIAA1058   GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
HC2E            GACGAGGAGGCCTCCATGATGGAAGACGTGGGGA-------------------------
HC2F            ------------------------------------------------------------

HC2A            GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG
HC2-80          GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG
HC2B            GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG
HC2C            GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG
HC2D-KIAA1058   GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG
HC2E            ----------------------------------------AAGCCGAGCGCTACGAG
HC2F            ------------------------------------------------------------

HC2A            CTCATCGCCGACATCTACAAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTT----
HC2-80          CTCATCGCCGACATCTACAAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTT----
HC2B            CTCATCGCCGACATCTACAAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTTTGAG
HC2C            CTCATCGCCGACATCTACAAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTTTGAG
HC2D-KIAA1058   CTCATTGCCGACATCTACAAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTTTGAG
HC2E            CTCATCGCCGACATCTACAAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTTTGAG
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
HC2C            AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
HC2D-KIAA1058   AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
HC2E            AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            CACTCGGGCCGCAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG-----
HC2C            CACTCGGGCCGCAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG-----
HC2D-KIAA1058   CACTCGGGCCGCAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGGCAGCG
HC2E            CACTCGGGCCGCAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG-----
HC2F            ------------------------------------------------------------

HC2A            ----------------------------------------CTTTGAAGATGAAGATGGA
HC2-80          ----------------------------------------CTTTGAAGATGAAGATGGA
HC2B            -------------------------------------GATTCTTTGAAGATGAAGATGGA
HC2C            -------------------------------------GATTCTTTGAAGATGAAGATGGA
HC2D-KIAA1058   CAATACCAGTTTACAGACAGTGAAACAGATGTGGAGGGATTCTTTGAAGATGAAGATGGA
HC2E            -------------------------------------GATTCTTTGAAGATGAAGATGGA
HC2F            ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC
HC2-80          AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC
HC2B            AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC
HC2C            AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC
HC2D-KIAA1058   AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC
HC2E            AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC
HC2F            ------------------------------------------------------------

HC2A            CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2-80          CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2B            CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2C            CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGACACAGGATTCTGGC
HC2D-KIAA1058   CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2E            CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2F            ------------------------------------------------------------

HC2A            AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2-80          AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2B            AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2C            AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2D-KIAA1058   AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCCTACATCCAGGTGACTCACGTCATC
HC2E            AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2F            ------------------------------------------------------------

HC2A            CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCACAAC
HC2-80          CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCACAAC
HC2B            CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCACAAC
HC2C            CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCACAAC
HC2D-KIAA1058   CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCACAAC
HC2E            CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCACAAC
HC2F            ------------------------------------------------------------

HC2A            ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2-80          ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2B            ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2C            ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2D-KIAA1058   ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2E            ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2F            ------------------------------------------------------------

HC2A            GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2-80          GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2B            GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2C            GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2D-KIAA1058   GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2E            GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2F            ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2-80          AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2B            AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2C            AAGCGCATCCCTTTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGT--CCATT
HC2D-KIAA1058   AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2E            AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2F            ------------------------------------------------------------

HC2A            GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2-80          GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2B            GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2C            GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2D-KIAA1058   GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2E            GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2F            ------------------------------------------------------------

HC2A            ATGATCAAACTGCAGCTCAAACTCCAGGGCAGCGTGAGTGTTCAGGTCAATGCTGGCCCA
HC2-80          ATGATCAAACTGCAGCTCAAACTCCAGGGCAGCGTGAGTGTTCAGGTCAATGCTGGCCCA
HC2B            ATGATCAAACTGCAGCTCAAACTCCAGGGCAGCGTGAGTGTTCAGGTCAATGCTGGCCCA
HC2C            ATGATCAAACTGCAGCTCAAACTCCAGGGCAGCGTGAGTGTTCAGGTCAATGCTGGCCCA
HC2D-KIAA1058   ATGATCAAACTGCAGCTCAAACTCCAGGGCAGCGTGAGTGTTCAGGTCAATGCTGGCCCA
HC2E            ATGATCAAACTGCAGCTCAAACTCCAGGGCAGCGTGAGTGTTCAGGTCAATGCTGGCCCA
HC2F            ------------------------------------------------------------

HC2A            CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2-80          CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2B            CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2C            CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2D-KIAA1058   CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2E            CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2F            ------------------------------------------------------------

HC2A            GTGAAGCTGCTTAAGGAAGTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2-80          GTGAAGCTGCTTAAGGAAGTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2B            GTGAAGCTGCTTAAGGAAGTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2C            GTGAAGCTGCTTAAGGAAGTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2D-KIAA1058   GTGAAGCTGCTTAAGGAAGTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2E            GTGAAGCTGCTTAAGGAAGTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2F            ------------------------------------------------------------

HC2A            GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2-80          GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2B            GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2C            GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2D-KIAA1058   GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2E            GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2F            ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG--------ATCTGCC
HC2-80          TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG--------ATCTGCC
HC2B            TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG--------ATCTGCC
HC2C            TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG--------ATCTGCC
HC2D-KIAA1058   TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAGCTGGGATGATCTGCC
HC2E            TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG--------ATCTGCC
HC2F            ------------------------------------------------------------

HC2A            CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2-80          CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2B            CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2C            CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2D-KIAA1058   CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2E            CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2F            ------------------------------------------------------------

HC2A            GGACTCCAACAAGCACAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2-80          GGACTCCAACAAGCACAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2B            GGACTCCAACAAGCACAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGA----
HC2C            GGACTCCAACAAGCACAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGA----
HC2D-KIAA1058   GGACTCCAACAAGCACAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2E            GGACTCCAACAAGCACAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGA----
HC2F            ------------------------------------------------------------

HC2A            ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTCATTTGCAAACTCAGGATGCTTTCCAA
HC2-80          ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTCATTTGCAAACTCAGGATGCTTTCCAA
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTCATTTGCAAACTCAGGATGCTTTCCAA
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA
HC2-80          AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCA-GGGGAAGGGGAGAGAAAGGAAA
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT
HC2-80          TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTCATTGTGTCTTAACAAAGGTGTGGTA
HC2-80          TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTCATTGTGTCTTAACAAAGGTGTGGTA
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTCATTGTGTCTTAACAAAGGTGTGGTA
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATG
HC2-80          GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATG
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATG
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            GCCTACAGAAAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2-80          GCCTACAGAAAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GCCTACAGAAAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            GCCTGGGGGACCTTTTGCCTCGACTCGTGCCGGAAATCTGATCGTAATCAGGGTACAGAA
HC2-80          GCCTGGGGGACCTTTTGCCTCGACTCGTGCCGGAAATCTGATCGTAATCAGGGTACAGAA
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   GCCTGGGGGACCTTTTGCCTCGAGGCTGAGCTGGAAAATCTTGAAAATATTTTTT----T
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            CTTACTAGTTTTGTCTAGGAGTATGTTGTATGACTAGGATTTGTGCTATTATCTCATTCA
HC2-80          CTTACTAGTTTTGTCTAGGAGTATGTTGTATGACTAGGATTTGTGCTATTATCTCATTCA
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TTTCCTGTGGCACATTCAGGTTGAATACAAGAACTATTTTTGTGACTAGTTTTTGATGAC
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAATCCGCTACTGG
HC2-80          ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAATCCGCTACTGG
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CTAAGGGAACTGACCATTGTAATTTTTGTACCAGTGAACCAGGAGATTTAGTGCTTTTAT
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A              CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2-80            CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2B              ------------------------------------------------------------
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     ATTCATTTCCTTGCATTTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAAACT
HC2E              ------------------------------------------------------------
HC2F              ------------------------------------------------------------

HC2A              TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAATTTGTG
HC2-80            TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAATTTGTG
HC2B              ------------------------------------------------------------
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     AGTCAAGCAGTTTAGAACCAAAGGCCTATATTAATAACCGCAACTATGCTGAAAAGTACA
HC2E              ------------------------------------------------------------
HC2F              ------------------------------------------------------------

HC2A              CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTCATAAAAATGTGCAATAT
HC2-80            CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTCATAAAAATGTGCAATAT
HC2B              ------------------------------------------------------------
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     AAGTAGTACAGTATATTGTTATGTACATATCATTGTTAATACAGTCCTGGCATTCTGTAC
HC2E              ------------------------------------------------------------
HC2F              ------------------------------------------------------------

HC2A              GGAGATGTATACAAGTCTTTACT-------------------------------------
HC2-80            GGAGATGTATACAAGTCTTTACT-------------------------------------
HC2B              ------------------------------------------------------------
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     ATATATGTATTACATTTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAAT
HC2E              ------------------------------------------------------------
HC2F              ------------------------------------------------------------

HC2A              ------------------------------------------------------------
HC2-80            ------------------------------------------------------------
HC2B              ------------------------------------------------------------
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     TGTGATAAATTTGTGCTGTTCCAGTATATGCAATACACTTTAATGTTTTATTCTTGTACA
HC2E              ------------------------------------------------------------
HC2F              ------------------------------------------------------------

HC2A              ------------------------------------------------------------
HC2-80            ------------------------------------------------------------
HC2B              ------------------------------------------------------------
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     TAAAAATGTGCAATATGGAGATGTATACAGTCTTTACTATATTAGGTTTATAAACAGTTT
HC2E              ------------------------------------------------------------
HC2F              ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TAAGAATTTCATCCTTTTGCCAAAATGGTGGAGTATGTAATTGGTAAATCATAAATCCTG
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TGGTGAATGGTGGTGTACTTTAAAGCTGTCACCATGTTATATTTTCTTTTAAGACATTAA
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TTTAGTAATTTTATATTTGGGAAAATAAAGGTTTTTAATTTTATTTAACTGGAATCACTG
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CCCTGCTGTAATTAAACATTCTGTACCACATCTGTATTAAAAAGACATTGCTGACC
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A              CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2-80            CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2B              ------------------------------------------------------------
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     ATTCATTTCCTTGCATTTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAAACT
HC2E              ------------------------------------------------------------
HC2F              ------------------------------------------------------------

HC2A              TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAATTTGTG
HC2-80            TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAATTTGTG
HC2B              ------------------------------------------------------------
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     AGTCAAGCAGTTTAGAACCAAAGGCCTATATTAATAACCGCAACTATGCTGAAAAGTACA
HC2E              ------------------------------------------------------------
HC2F              ------------------------------------------------------------

HC2A              CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTCATAAAAATGTGCAATAT
HC2-80            CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTCATAAAAATGTGCAATAT
HC2B              ------------------------------------------------------------
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     AAGTAGTACAGTATATTGTTATGTACATATCATTGTTAATACAGTCCTGGCATTCTGTAC
HC2E              ------------------------------------------------------------
HC2F              ------------------------------------------------------------

HC2A              GGAGATGTATACAAGTCTTTACT-------------------------------------
HC2-80            GGAGATGTATACAAGTCTTTACT-------------------------------------
HC2B              ------------------------------------------------------------
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     ATATATGTATTACATTTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAAT
HC2E              ------------------------------------------------------------
HC2F              ------------------------------------------------------------

HC2A              ------------------------------------------------------------
HC2-80            ------------------------------------------------------------
HC2B              ------------------------------------------------------------
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     TGTGATAAATTTGTGCTGTTCCAGTATATGCAATACACTTTAATGTTTTATTCTTGTACA
HC2E              ------------------------------------------------------------
HC2F              ------------------------------------------------------------

HC2A              ------------------------------------------------------------
HC2-80            ------------------------------------------------------------
HC2B              ------------------------------------------------------------
HC2C              ------------------------------------------------------------
HC2D-KIAA1058     TAAAAATGTGCAATATGGAGATGTATACAGTCTTTACTATATTAGGTTTATAAACAGTTT
HC2E              ------------------------------------------------------------
HC2F              ------------------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TAAGAATTTCATCCTTTTGCCAAAATGGTGGAGTATGTAATTGGTAAATCATAAATCCTG
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TGGTGAATGGTGGTGTACTTTAAAGCTGTCACCATGTTATATTTTCTTTTAAGACATTAA
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   TTTAGTAATTTTATATTTGGGAAAATAAAGGTTTTTAATTTTATTTAACTGGAATCACTG
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------------------

HC2A            ------------------------------------------------------------
HC2-80          ------------------------------------------------------------
HC2B            ------------------------------------------------------------
HC2C            ------------------------------------------------------------
HC2D-KIAA1058   CCCTGCTGTAATTAAACATTCTGTACCACATCTGTATTAAAAAGACATTGCTGACC
HC2E            ------------------------------------------------------------
HC2F            ------------------------------------------------
```

FIG. 3A (cont.)

```
HC2A      ------------------------------------------------------------
HC2A-80   ------------------------------------------------------------
HC2B      ------------------------------------------------------------
HC2C      ------------------------------------------------------------
HC2D      ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
HC2E      ------------------------------------------------------------
HC2F      ------------------------------------------------------------

HC2A      ------------------------------------------------------------
HC2A-80   ------------------------------------------------------------
HC2B      ------------------------------------------------------------
HC2C      ------------------------------------------------------------
HC2D      FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
HC2E      ------------------------------------------------------------
HC2F      ------------------------------------------------------------

HC2A      ----------------------------------------------VLHHHQNPEFYDEIK
HC2A-80   ------------------------------------------------------------
HC2B      ------------------------------------------------------------
HC2C      ------------------------------------------------------------
HC2D      KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
HC2E      ------------------------------------------------------------
HC2F      ------------------------------------------------------------

HC2A      IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
HC2A-80   ------------------------------------------------------------
HC2B      ------------------------------------------------------------
HC2C      ------------------------------------------------------------
HC2D      IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
HC2E      ------------------------------------------------------------
HC2F      ------------------------------------------------------------

HC2A      PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
HC2A-80   ------------------------------------------------------------
HC2B      ------------------------------------------------------------
HC2C      ------------------------------------------------------------
HC2D      PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
HC2E      ------------------------------------------------------------
HC2F      ------------------------------------------------------------

HC2A      QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2A-80   ------------------------------------------------------------
HC2B      ----------------------AMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2C      ------------------------------------------------------------
HC2D      QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2E      ----------------------AMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2F      ------------------------------------------------------------
```

Fig. 3B

```
HC2A      IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2A-80   ------------------------------------------------------------
HC2B      IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2C      ------------------------------------------------------------
HC2D      IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2E      IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2F      ------------------------------------------------------------

HC2A      LLRYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAAETVVNMLMPHITQKFGDN
HC2A-80   ------------------------------------------------------------
HC2B      LLRYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAAETVVNMLMPHITQKFGDN
HC2C      ------------------------------------------------------------
HC2D      LLKYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAVETVVNMLMPHITQKFRDN
HC2E      LLRYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAAETVVNMLMPHITQKFGDN
HC2F      ------------------------------------------------------------

HC2A      PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2A-80   ------------------------------------------------------------
HC2B      PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2C      ------------------------------------------------------------
HC2D      PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2E      PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2F      ------------------------------------------------------------

HC2A      EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTALQEFREVRLI
HC2A-80   ----------------------QLDYSLTDEFCRNHFLVGLLLREVGTALQEFREVRLI
HC2B      EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTALQEFREVRLI
HC2C      ------------------------------------------------------------
HC2D      EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTALQEFREVRLI
HC2E      EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTALQEFREVRLI
HC2F      ------------------------------------------------------------

HC2A      AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2A-80   AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2B      AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2C      ------------------------------------------------------------
HC2D      AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2E      AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2F      ------------------------------------------------------------

HC2A      VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2A-80   VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2B      VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2C      ------------------------------------------------------------
HC2D      VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2E      VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2F      ----------------------------------------------------ADSRGS
```

FIG. 3B (cont.)

```
HC2A      LISTDSGNSLPERNSEKSNSLDKHQQSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2A-80   LISTDSGNSLPERNSEKSNSLDKHQQSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2B      LISTDSGNSLPERNSEKSNSLDKHQQSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2C      ------------------------------------------------------------
HC2D      LISTDSGNSLPERNSEKSNSLDKHQQSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2E      LISTDSGNSLPERNSEKSNSLDKHQQSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2F      LISTDSGNSLPERNSEKSNSLDKHQQSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS

HC2A      DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDRKSQTLPVS
HC2A-80   DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDRKSQTLPVS
HC2B      DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDRKSQTLPVS
HC2C      ------------------------------------------------------------
HC2D      DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIAR--------------------
HC2E      DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGLGPIVHDRKSQTLPVS
HC2F      DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIAS-------VR--KISSVLGIS

HC2A      RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2A-80   RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2B      RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2C      ------------------------------------------------------------
HC2D      ---TGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2E      RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2F      V----------------D-NG-----YGHSDADVLHQSLLEANIATEVCLTALDTLSLFT

HC2A      LAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2A-80   LAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2B      LAFK--LLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2C      ------------------------------------------------------------
HC2D      LAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2E      LAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2F      LAFKNQLLADHGHNPLMKKK------------------------------------------

HC2A      DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQLI
HC2A-80   DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQLI
HC2B      DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQLI
HC2C      ------------------------------------------------------------
HC2D      DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQLI
HC2E      DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQLI
HC2F      ------------------------------------------------------------

HC2A      ADVVGIGETRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2A-80   ADVVGIGETRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2B      ADVVGIGETRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2C      ------------------------------------------------------------
HC2D      ADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2E      ADVVGIGETRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2F      ------------------------------------------------------------
```

FIG. 3B (cont.)

```
HC2A      PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHVTALVAEYLTRK
HC2A-80   PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHVTALVAEYLTRK
HC2B      PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHVTALVAEYLTRK
HC2C      ------------------------------------------------------------
HC2D      PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHVTALVAEYLTRK
HC2E      PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHVTALVAEYLTRK
HC2F      ------------------------------------------------------------

HC2A      ----------------------GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2A-80   ----------------------GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2B      ----------------------GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2C      -----------------------FRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2D      EAVQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2E      ----------------------GVFRQGCTAFRVITPNIDEEASMMEDVG--------
HC2F      ------------------------------------------------------------

HC2A      DVLMELLEQCADGLWKAERYELIADIYKLIIPIYEKRR------------------
HC2A-80   DVLMELLEQCADGLWKAERYELIADIYKLIIPIYEKRR------------------
HC2B      DVLMELLEQCADGLWKAERYELIADIYKLIIPIYEKRRDFERLAHLYDTLHRAYSK
HC2C      DVLMELLEQCADGLWKAERYELIADIYKLIIPIYEKRRDFERLAHLYDTLHRAYSK
HC2D      DVLMELLEQCADGLWKAERYELIADIYKLIIPIYEKRRDFERLAHLYDTLHRAYSK
HC2E      ---------------KAERYELIADIYKLIIPIYEKRRDFERLAHLYDTLHRAYSK
HC2F      ------------------------------------------------------------

HC2A      ------------------------------------DFFEDEDGKEYIYKEPKLTPLSE
HC2A-80   ------------------------------------DFFEDEDGKEYIYKEPKLTPLSE
HC2B      VTEVMHSGRRLLGTYFRVAFFG--------------QGFFEDEDGKEYIYKEPKLTPLSE
HC2C      VTEVMHSGRRLLGTYFRVAFFG--------------QGFFEDEDGKEYIYKEPKLTPLSE
HC2D      VTEVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVEGFFEDEDGKEYIYKEPKLTPLSE
HC2E      VTEVMHSGRRLLGTYFRVAFFG--------------QGFFEDEDGKEYIYKEPKLTPLSE
HC2F      ------------------------------------------------------------

HC2A      ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF
HC2A-80   ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF
HC2B      ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF
HC2C      ISQRLLKLYSDKFGSENVKMTQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF
HC2D      ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF
HC2E      ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF
HC2F      ------------------------------------------------------------

HC2A      ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2A-80   ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2B      ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2C      ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPFMYQHHTDLNP
HC2D      ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2E      ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2F      ------------------------------------------------------------
```

FIG. 3B (cont.)

```
HC2A        IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR
HC2A-80     IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR
HC2B        IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR
HC2C        IEVHZ-----------------------------------------------------
HC2D        IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR
HC2E        IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR
HC2F        ------------------------------------------------------------

HC2A        YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2A-80     YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2B        YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2C        ------------------------------------------------------------
HC2D        YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2E        YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2F        ------------------------------------------------------------

HC2A        ICPLEEKTSVLPNSLHIFNAISGTPTSTMVHGMTSSSSVVZ-----
HC2A-80     ICPLEEKTSVLPNSLHIFNAISGTPTSTMVHGMTSSSSVVZ-----
HC2B        ICPLEEKTSVLPNSLHIFNAISGTPTSTMVHGMTSSSSVVZ-----
HC2C        ---------------------------------------------
HC2D        LG-----------------------------------------------
HC2E        ICPLEEKTSVLPNSLHIFNAISGTPTSTMVHGMTSSSSVVZ-----
HC2F        ---------------------------------------------
```

FIG. 3B (cont.)

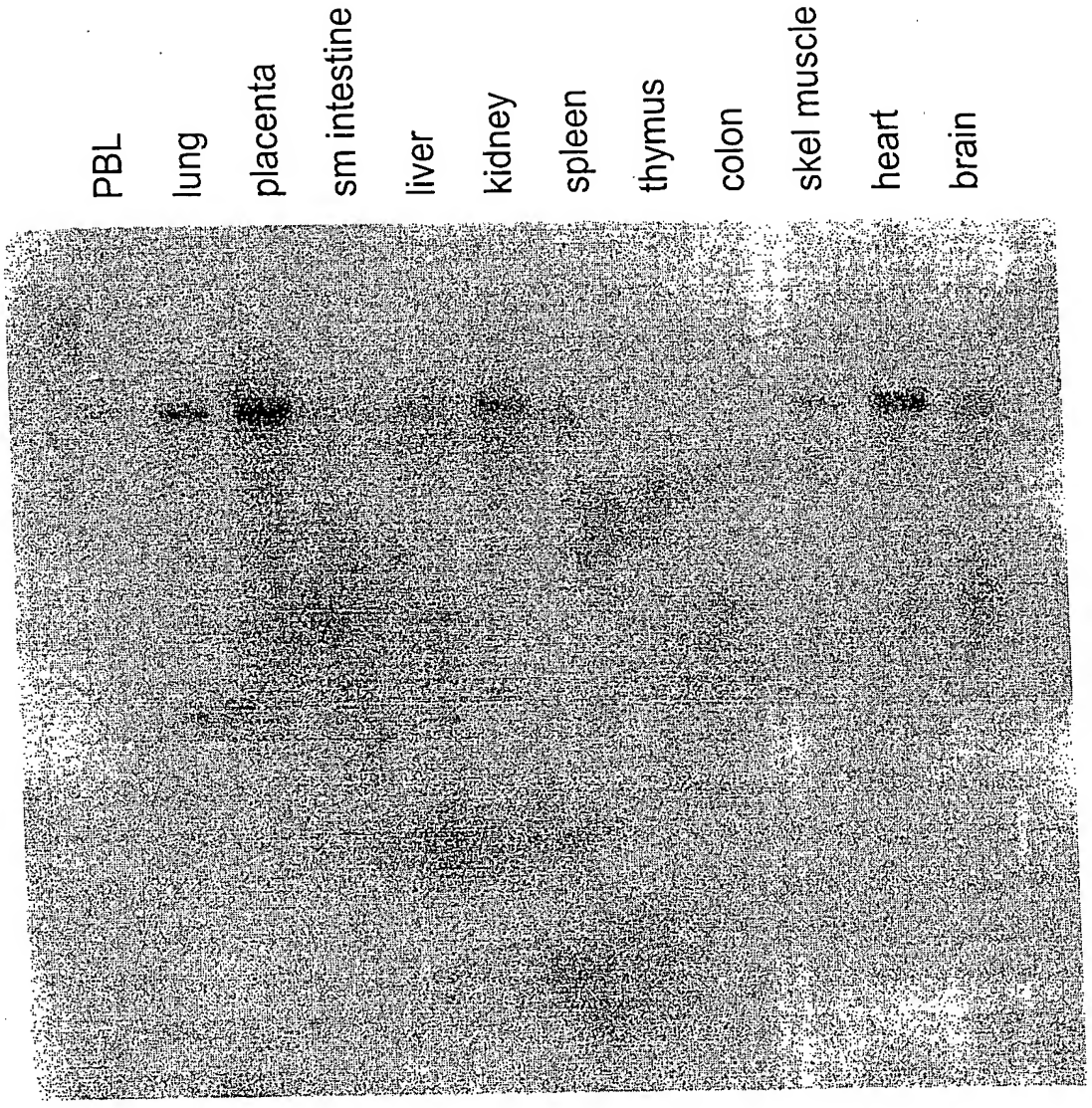

PBL
lung
placenta
sm intestine
liver
kidney
spleen
thymus
colon
skel muscle
heart
brain

FIG. 4A

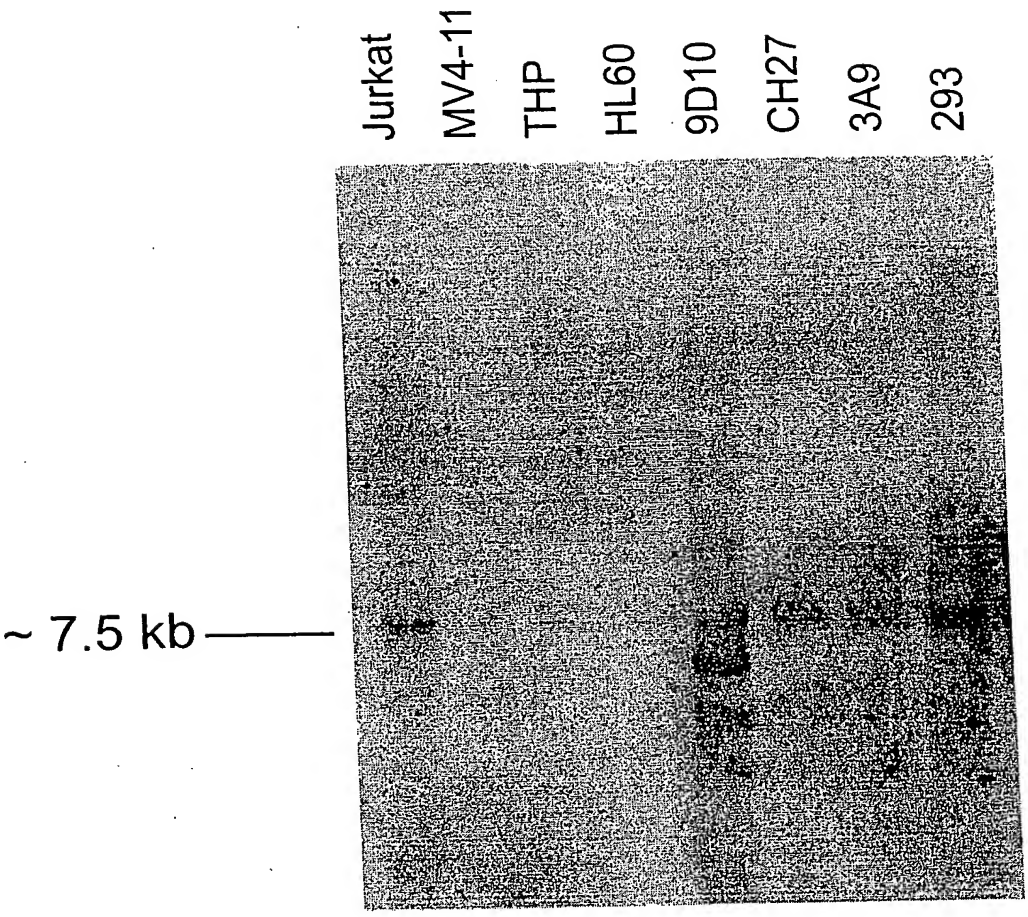


FIG. 4B

```
HC2A  ------------------------------------------------------------
KIAA  ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat   ------------------------------------------------------------
HC4   ------------------------------------------------------------
HC1   ------------------------------------------------------------
HC3   ------------------------------------------------------------
HC5   ------------------------------------------------------------

HC2A  ------------------------------------------------------------
KIAA  FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat   ------------------------------------------------------------
HC4   ------------------------------------------------------------
HC1   ------------------------------------------------------------
HC3   ------------------------------------------------------------
HC5   ------------------------------------------------------------

HC2A  ----------------------------------------------VLHHHQNPEFYDEIK
KIAA  KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
rat   ------------------------------------------------------------
HC4   ------------------------------------------------------------
HC1   ------------------------------------------------------------
HC3   ------------------------------------------------------------
HC5   ------------------------------------------------------------

HC2A  IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA  IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat   ------------------------------------------------------------
HC4   ------------------------------------------------------------
HC1   ------------------------------------------------------------
HC3   ------------------------------------------------------------
HC5   ------------------------------------------------------------

HC2A  PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA  PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat   ------------------------------------------------------------
HC4   ------------------------------------------------------------
HC1   ------------------------------------------------------------
HC3   ----------------------------------------GPGPARSTVSISLISNSARV
HC5   ------------------------------------------------------------

HC2A  QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA  QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat   ------------------------------------------------------------
HC4   ----------------------MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1   --------------------------MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3   NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5   ------------------------------------------------------------
```

FIG.5A

```
HC2A    IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
KIAA    IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
rat     ------------------------------------------------------------
HC4     LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1     LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVHEDLAKNVTGLLK-SNDSPTVK
HC3     TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E
HC5     ------------------------------------------------------------

                                        Cadherin
                                        Cleavage
HC2A    KLLRYSWFFFDVLIKSMAQHLIENSKVKLIRNQRFPASYHHAAETVVNMLMPHITQKFGD
KIAA    KLLKYSWFFFDVLIKSMAQHLIENSKVKLIRNQRFPASYHHAVETVVNMLMPHITQKFRD
rat     ------------------------------------------------------------
HC4     KLLKYSWFFFEIIAKSMATYLLEENKIKLTHGQRFPKAYHHALHSLFLAIT-IVESQYAE
HC1     HVLKHSWFFFAIILKSMAQHLIDTNKIQLERPQRFPESYQNELDNLVMVLSDHVIWKYKD
HC3     SALQQAWFFFELMVKSMVHHLYFNDKLEAERKSRFPERFMDDIAALVSTIASDIVSRFQK
HC5     ------------------------------------------------------------

HC2A    NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA    NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat     ------------------------------------------------------------
HC4     IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1     ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLCQYKFDFL
HC3     DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFL
HC5     ------------------------------------------------------------

HC2A    RVVCNHEHYIPLNLPM-----PFGKGRIQR------------YQDLQL----DYSLTDEF
KIAA    RVVCNHEHYIPLNLPM-----PFGKGRIQR------------YQDLQL----DYSLTDEF
rat     ------------------------------------------------------------
HC4     QTICNHEHYIPLNLPM-----AFAKPKLQR------------VQDSNL----EYSLSDEY
HC1     QEVCQHEHFIPLCLPIRSANIPDPLTPSES------------TQELHASDMPEYSVTNEF
HC3     RIICSHEHYVTLNLPCSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5     ---------------MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA

HC2A    CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA    CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat     ------------------------------------------------------------
HC4     CKHHFLVGLLLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAKIAQ
HC1     CRKHFLIGILLREVGFALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
HC3     RQQHYLAGLVLTELAVILDPDAEGLFGLHKKVINMVHNLLSSHDSDPRYSDPQIKARVAM
HC5     SSTS-SPGLLFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAA

HC2A    LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA    LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat     ------------------------------------------------------------
HC4     LYLPFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1     LYMPLYGMLLDNMPRIYLKDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFS
HC3     LYLPLIGIIMETVPQLYDFTETHNQRGRPICIATDDYESE-----------SG---SMIS
HC5     LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----------GA---GAIT

HC2A    KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS
KIAA    KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS
rat     ------------------------------------------------------------
HC4     TDKDTAYGSFQNG--------HGIKREDSRGSLIP-EGATGFPDQGNTGEN-----TRQS
HC1     KDVLNSIAAFSS------IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
HC3     QTVAMAIAGTSVPQ-------------------LTRPGSFLLTSTSGRQHT---------
HC5     QNVALAIAGNNFN--------------------LKTSG-IVLSSLPYKQYN---------
```

FIG. 5A (cont.)

```
HC2A    TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
KIAA    TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
rat     ------------------------------------------------------------
HC4     STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLLTYWN-KVSPQELINILILLEVCL
HC1     ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3     ----------TFSAESSRSLLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLLDLLYLCV
HC5     ----------MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A    HQFQYMGKRYIARNQEGLG--PIVHDRKS------------------QTLPVSRNRTGMM
KIAA    HQFQYMGKRYIAR-----------------------------------------TGMM
rat     ------------------------------------------------------------
HC4     FHFRYMGKRNIARVHDAWLSKHFGIDRKS------------------QTMPALRNRSGVM
HC1     QNFRYLGKRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK
HC3     SCFEYKGKKVFERMNSLTFK--KSKDMRAK--------------LEEAILGSIGARQEMV
HC5     LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR--------------LEEALLRGEGARGEMM

HC2A    HARLQQL---------GSLDNS---------LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA    HARLQQL---------GSLDNS---------LTFNHSYGHSDADVLHQSLLEANIATEVC
rat     ------------------------------------------------------------
HC4     QARLQHL---------SSLESS---------FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1     QHRSQTLPIIRGK---NALSNPKL----LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC
HC3     RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTEKLDKSRAEIEHEALIDGNLATEAN
HC5     RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A    LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
KIAA    LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
rat     ----------------KLSRGHSPLMKKVFDVYLCFLQKHQSEMALKNVFTALRSLIY
HC4     LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1     LTILDLVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNQSATALKHVFASLRLFVC
HC3     LIILDTLEIVVQTVS--VTES--KESILGGVLKVLLHSMACNQSAVYLQHCFATQRALVS
HC5     LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDQSTTYLTHCFATLRALIA

HC2A    KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
KIAA    KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
rat     KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC4     KFPSAFFKGRVNMCAAFCYEVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1     KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3     KFPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK
HC5     KFGDLLFEEEVEQCFDLCHQVLHHCSSSMDVTRSQACATLYLLMRFSFGATS--NFARVK

HC2A    LQVIISVSQLIADVVGIGETRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
KIAA    LQVIISVSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
rat     LQVIISLSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
HC4     LQIIIAVSQLIADVALSGGSRFQESLFIINNFANSDRPMLARAFPAEVKDLTKRIRTVLM
HC1     LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM
HC3     MQVPMSLSSLVGTSQNFNEEFLRRSLKTILTYAEEDLELRETTFPDQVQDLVFNLHMILS
HC5     MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTPFPTQVEELLCNLNSILY
```

FIG. 5A (cont.)

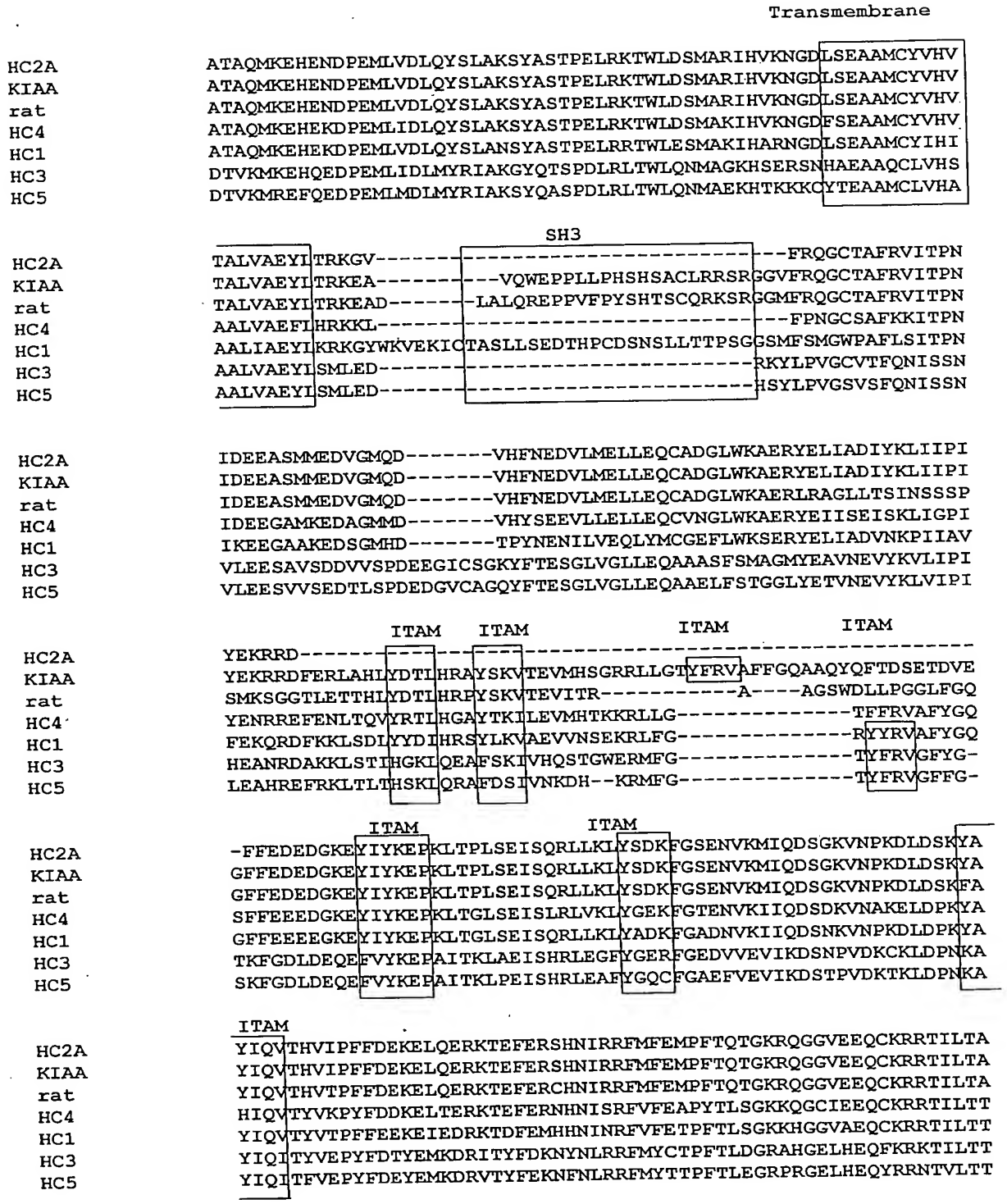

Transmembrane
HC2A ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
KIAA ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
rat ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
HC4 ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLDSMAKIHVKNGDFSEAAMCYVHV
HC1 ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHI
HC3 DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPDLRLTWLQNMAGKHSERSNHAEAAQCLVHS
HC5 DTVKMREFQEDPEMLMDLMYRIAKSYQASPDLRLTWLQNMAEKHTKKKCYTEAAMCLVHA
SH3
HC2A TALVAEYLTRKGV---FRQGCTAFRVITPN
KIAA TALVAEYLTRKEA---VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat TALVAEYLTRKEAD---LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4 AALVAEFLHRKKL---FPNGCSAFKKITPN
HC1 AALIAEYLKRKGYWKVEKICTASLLSEDTHPCDSNSLLTTPSGGSMFSMGWPAFLSITPN
HC3 AALVAEYLSMLED---RKYLPVGCVTFQNISSN
HC5 AALVAEYLSMLED---HSYLPVGSVSFQNISSN
HC2A IDEEASMMEDVGMQD---VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIPI
KIAA IDEEASMMEDVGMQD---VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIPI
rat IDEEASMMEDVGMQD---VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4 IDEEGAMKEDAGMMD---VHYSEEVLLELLEQCVNGLWKAERYEIISEISKLIGPI
HC1 IKEEGAAKEDSGMHD---TPYNENILVEQLYMCGEFLWKSERYELIADVNKPIIAV
HC3 VLEESAVSDDVVSPDEEGICSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLIPI
HC5 VLEESVVSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIPI
ITAM ITAM ITAM ITAM
HC2A YEKRRD---
KIAA YEKRRDFERLAHLYDTLHRAYSKVTEVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVE
rat SMKSGGTLETTHLYDTLHRPYSKVTEVITR---A----AGSWDLLPGGLFGQ
HC4 YENRREFENLTQVYRTLHGAYTKILEVMHTKKRLLG---TFFRVAFYGQ
HC1 FEKQRDFKKLSDLYYDIHRSYLKVAEVVNSEKRLFG---RYYRVAFYGQ
HC3 HEANRDAKKLSTIHGKLQEAFSKIVHQSTGWERMFG---TYFRVGFYG-
HC5 LEAHREFRKLTLTHSKLQRAFDSIVNKDH--KRMFG---TYFRVGFFG-
ITAM ITAM
HC2A -FFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
KIAA GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
rat GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA
HC4 SFFEEEDGKEYIYKEPKLTGLSEISLRLVKLYGEKFGTENVKIIQDSDKVNAKELDPKYA
HC1 GFFEEEEGKEYIYKEPKLTGLSEISQRLLKLYADKFGADNVKIIQDSNKVNPKDLDPKYA
HC3 TKFGDLDEQEFVYKEPAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA
HC5 SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGQCFGAEFVEVIKDSTPVDKTKLDPNKA
ITAM
HC2A YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4 HIQVTYVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLSGKKQGCIEEQCKRRTILTT
HC1 YIQVTYVTPFFEEKEIEDRKTDFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILTT
HC3 YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGELHEQFKRKTILTT
HC5 YIQITFVEPYFDEYEMKDRVTYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTT

FIG. 5A (cont.)

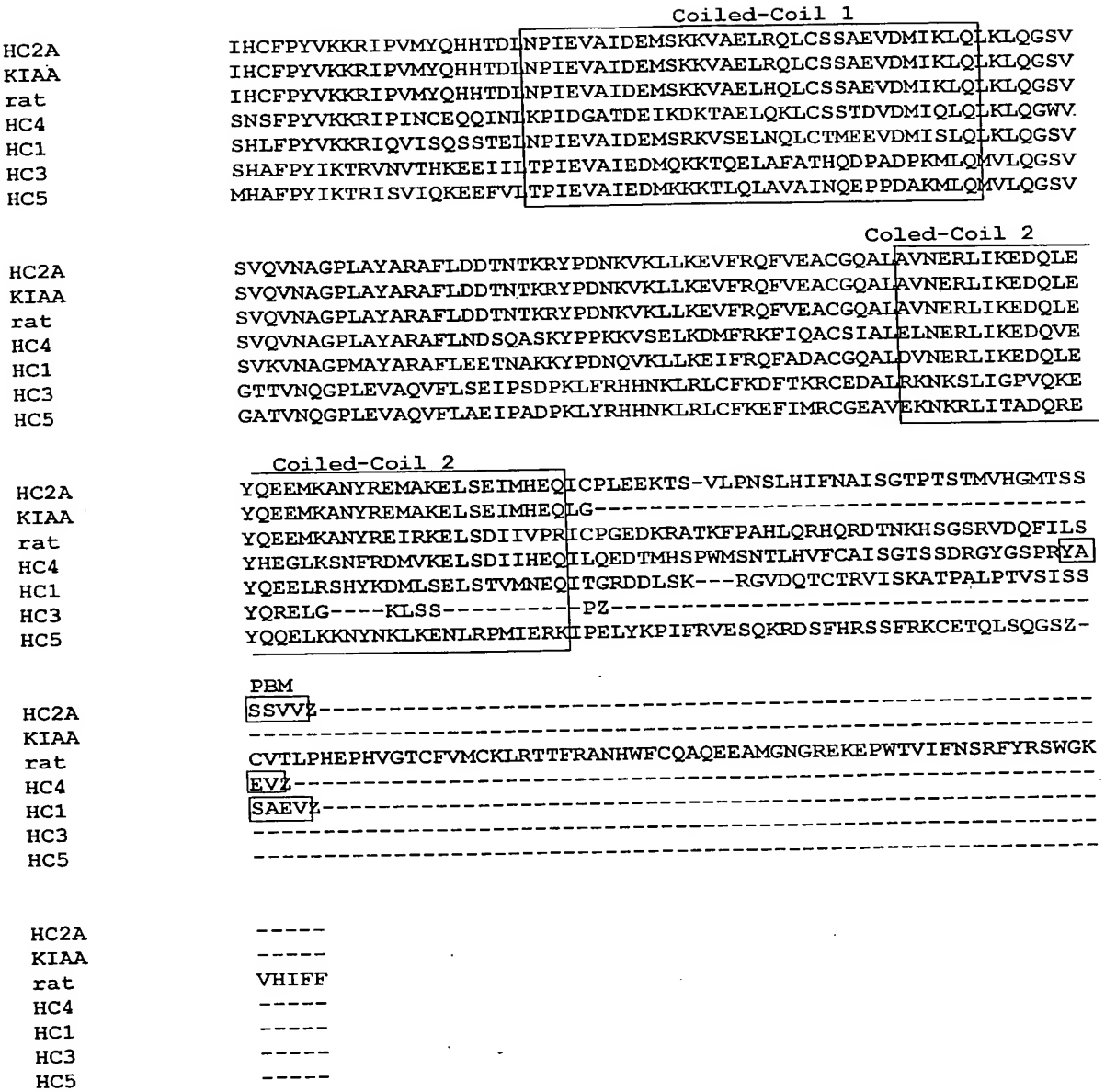

Coiled-Coil 1
HC2A IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV
HC4 SNSFPYVKKRIPINCEQQINLKPIDGATDEIKDKTAELQKLCSSTDVDMIQLQLKLQGWV
HC1 SHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3 SHAFPYIKTRVNVTHKEEIILTPIEVAIEDMQKKTQELAFATHQDPADPKMLQMVLQGSV
HC5 MHAFPYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPDAKMLQMVLQGSV
Coled-Coil 2
HC2A SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
KIAA SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
rat SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
HC4 SVQVNAGPLAYARAFLNDSQASKYPPKKVSELKDMFRKFIQACSIALELNERLIKEDQVE
HC1 SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALQVNERLIKEDQLE
HC3 GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE
HC5 GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE
Coiled-Coil 2
HC2A YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPTSTMVHGMTSS
KIAA YQEEMKANYREMAKELSEIMHEQLG----------
rat YQEEMKANYREIRKELSDIIVPRICPGEDKRATKFPAHLQRHQRDTNKHSGSRVDQFILS
HC4 YHEGLKSNFRDMVKELSDIIHEQILQEDTMHSPWMSNTLHVFCAISGTSSDRGYGSPRYA
HC1 YQEELRSHYKDMLSELSTVMNEQITGRDDLSK---RGVDQTCTRVISKATPALPTVSISS
HC3 YQRELG----KLSS----------PZ----------
HC5 YQQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGSZ-
PBM
HC2A SSVVZ----------
KIAA ----------
rat CVTLPHEPHVGTCFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGK
HC4 EVZ----------
HC1 SAEVZ----------
HC3 ----------
HC5 ----------
HC2A -----
KIAA -----
rat VHIFF
HC4 -----
HC1 -----
HC3 -----
HC5 -----

FIG. 5A (cont.)

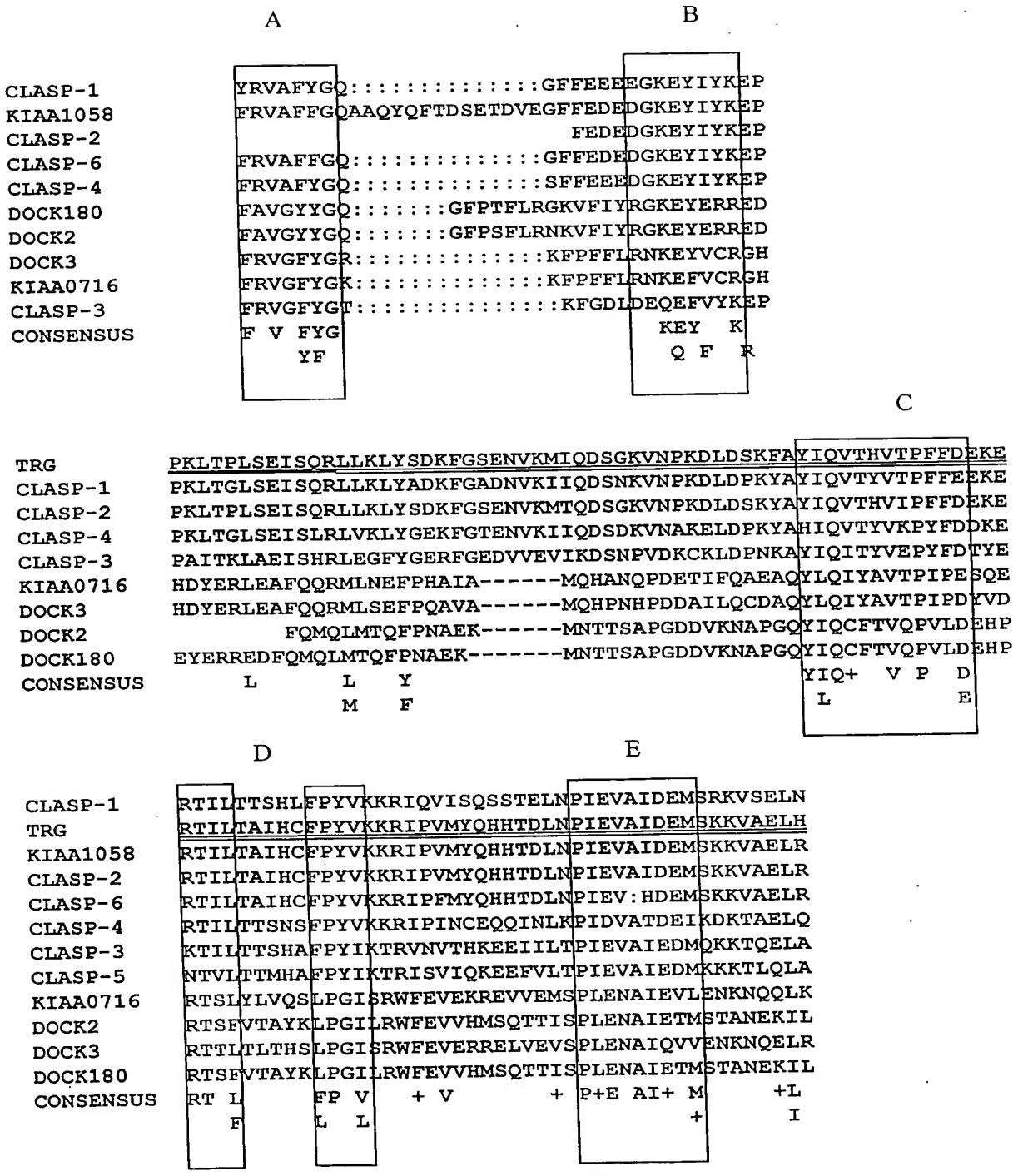
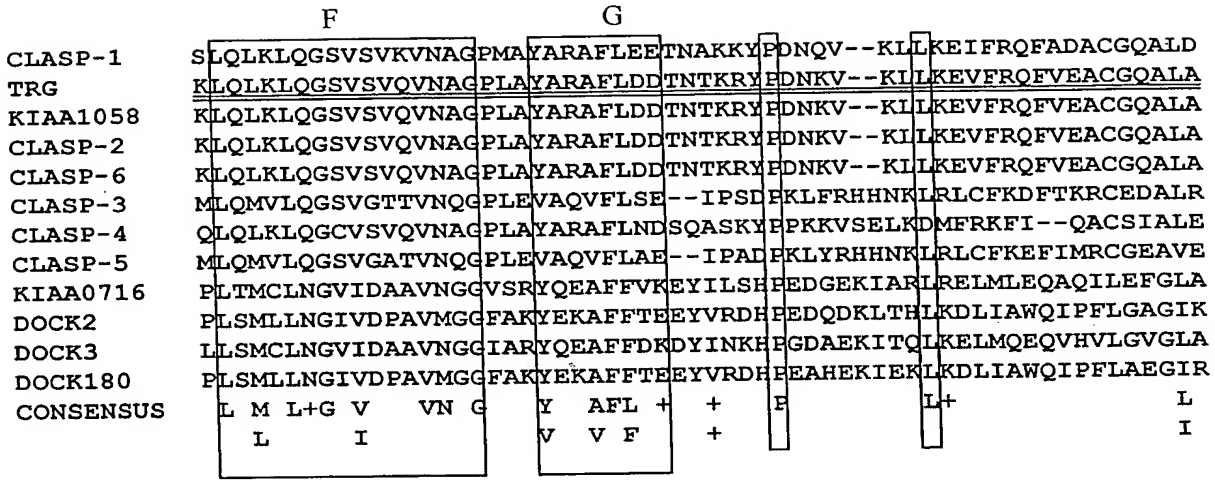

A
B
CLASP-1
KIAA1058
CLASP-2
CLASP-6
CLASP-4
DOCK180
DOCK2
DOCK3
KIAA0716
CLASP-3
CONSENSUS
C
TRG
CLASP-1
CLASP-2
CLASP-4
CLASP-3
KIAA0716
DOCK3
DOCK2
DOCK180
CONSENSUS
D
E
CLASP-1
TRG
KIAA1058
CLASP-2
CLASP-6
CLASP-4
CLASP-3
CLASP-5
KIAA0716
DOCK2
DOCK3
DOCK180
CONSENSUS

FIG. 5B



DOCK2=KIAA0209
DOCK3=KIAA0299
CLASP2variant=KIAA1058

FIG. 5B (cont.)

1
A

```
2                                                  32
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62                                                 92
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122                                                152
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182                                                212
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242                                                272
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302                                                332
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr
                ref 1.1, 1.2 and 1.3
362                                                392
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422                                                452
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482                                                512
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542                                                572
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602                                                632
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662                                                692
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met
```

FIG. 6A

```
722                                                 752
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782                                                 812
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842              |Cadherin Cleavage|          872
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902                                                 932
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962                                                 992
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly
                                                                    ref 2.1
1022                                                1052
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082                                                1112
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142                                                1172
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202                                                1232
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

1262                                                1292
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu
                                                                    ref 3.1
1322                                                1352
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382                                                1412/471
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442                                                1472
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser
```

FIG. 6A (cont.)

```
1502                                                1532
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn
                                                    ref 4.1 and 4.2
1562                                                1592
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622                                                1652
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp
                                                    ref 5.1 and 5.2
1682                                                1712
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742                                                1772
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802                                                1832
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862                                                1892
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val
                    ref 6.1
1922                                                1952
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982                                                2012
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042                                                2072
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102                                                2132
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

                                                                    ref 7.1
2162                                                2192
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

2222                                                2252
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

2282                                                2312
```

FIG. 6A (cont.)

```
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342                                        2372
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402                                        2432
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462                                        2492
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522                                        2552
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582                                        2612
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642                                        2672
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702                                        2732
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762                                        2792
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822                                        2852        |xxxxxxxxxxxxxxx Predicted
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

Transmembrane Domain xxxxxxxxxxxxxxxxxxxxxxxxxxx|
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942                                        2972
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu
    ref 8.1
3002                                        3032
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062                                        3092
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT
cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu
```

FIG. 6A (cont.)

```
                                    ref 9.1
                                    ⇩
3122                                3152
ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT
ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182                                3212
ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG
ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu
                                                          ref 10.1
                                                          ⇩
3242                                3272
TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC
tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302                                3332
CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT
pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362                                3392
GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC
asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422                                3452
TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG
phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln
                ref 11.1
                ⇩
3482                                3512
TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC
cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys lys arg ile

3542                                3572    |xxxxxxxx Coiled-coil 1 xxxxxx
CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG
pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

3602 xxxxxxxx Coiled coil 1 cont'd xxxx 3632 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA
ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys
                                        ref 12.1
                                        ⇩
3662 xxxxxxxxxxxxxxxxxxxxxx |           3692
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722                                3752
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782                                3812                |xxxxxxxxxxxxxxxxx
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

3842 xxxxxxx Coiled coil 2 xxxxxxxxxx 3872 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

3902 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx 3932 xxx|
```

FIG. 6A (cont.)

```
ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962                                          3992
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022                                |xxxx PBM xxxxx|
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG
met val his gly met thr ser ser ser ser val val STP

4082                                          4112
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142                                          4172
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202                                          4232
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262                                          4292
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322                                          4352
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382                                          4412
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

                ⇩ ref 13.1
4442                                          4472
CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502                                          4532
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562                                          4592
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT
                                                  ⇩ ref 14.1
4622                                          4652
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682                                          4712
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742                                          4772
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802
TTT ACT
```

FIG. 6A (cont.)

BAC sequences of Human CLASP 2

Ref 1.1
Sequence of BAC4 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 356-375.

TTTCTACAGNGTNTACTCAGGTATGTGCTCCTTCAACAAAATTAGCAGTTGCTGCTCT
GTGACAAAGTTTGCACCATTTTGCAAGAAGAAAAAAATCCTAATGTGTTATATTACTA
TATTTTTACTCTATAGATCTTTTTCTAAAGAAAGAAAGTACAACTGAAGTGCTTATAT
GTATTCATATAAATGACTAGTACAAGCATCATTTTGCAACAGATTTCCCCTTTCATTG
GAGGATCTTCTTGATGTTATTTGTACACGATCAATTTTTAGTCTTAATAAGATGAGGC
TGGGTGTGGTGGCTCACACCTGTAATCCTAGCATTTTGGAGGCCAAGGTGGGCAGAT
CACTTTAGCCCAGGGGTTTGAGACCAGCCTGGCCAACATGGCAAAACCTTGTCTCTA
CAAAAATACNAAAATTATCCAGGCATGGTGATGTGTGCCTGTAGTCCCAACTNCCTAG
GAGGCTAGGGGTAGGGGGATTTGCAAGAGGCTGGGAGGGTCAAAGCCCNAANTGAG
CCATTGGTNCATGTCACTTGGACCCCAAGCNNGGGGNGANCAAGAGCAAAGGACTNN
TGTNNTTTANAAAAAAAACCGGGCTACCATACNNACCAACCCNCNNACCTACCCNACC
TTTCCANNTTAAAANAAGGCTTTGNCTTGCANAGGAAAANCAAAATNNCC

Ref 1.2
Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 351-375.

TCTGGTTTCTACAGTGTATACTNAGGTATGTGCTCCTTNAACAAAATTAGCAGTTGCT
GCTCTGTGACAAAGTTTGCACCATTTTGCAAGAAGAAAAAAATCCTAATGTGTTATAT
TACTATATTTTTACTCTATAGATCTTTTTCTAAAGAAAGAAAGTACAACTGAAGTGCTT
ATATGTATTCATATAAATGACTAGTACAAGCATCATTTTGCAACAGATTTCCCCTTTC
ATTGGAGGATCTTCTTGATGTTATTTGTACACGATCAATTTTTAGTCTTAATAAGATG
AGGCTGGGTGTGGTGGCTCACACCTGTAATCCTAGCATTTTGGAGGCCAAGGTGGGC
AGATCACTTTAGCCCAGGGGTTTGAGACCAGCCTGGCCAACATGGCAAAACCTTGTC
TCTACAAAAATACAAAAATTATCCAGGCATGGTGATGTGTGCCTGTAGTCCCAGCTAC
CTAGGAGGCTAGGGTAGGGGGATTGCAAGAGGCTNGGAGGTCAAGGCCCGCAGTGA
GCCATGGTCATGTCACTGCACCCCCAGCCAGGGCCGACAGGAGCAAGACTNTTGTNT
CAAAAAAAAACAGNAACCAACANCCAACAACAACAACNACCTTTCNGCAAAANAAGC
TTGCTNCAANGAAACCAAAATGNCTTCTTNTTTTCCCCCN

Ref 1.3
Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is not found within this sequence. This sequence most likely represent intron sequence since this sequence matches the intron sequence found in the previous two BAC sequences.

AGNNNNNCCCNCTACNCCACTTTTAACCTTTTGAAAACACAGTGTTTNCTCAANTATG
CGCTCCTTCACATATTAGCAGTTGCTGCTCTGTGACATAGTTGCACCATTNTGCAAGA
AGAAAAAATCCTAAGTGTNATATCACTATATNNNTACTCTATAGATCTTNTCTAAAGA
AAGAAAGTCAACTGATGTGCTTATATGTATNCATATAAATGACTAGTACATGCATCAT
TTTGCAACAGATNTCTCCTCACATTGGAGGATCTTCTNGANGNATTCGACACGATNAN
TATTAGTCTNAATAAGATGANGCTGGTGTGGNGGTACACTGNATCTAGCATNTGGAN
GCATGTGGCAGACACTTANCCNCGGTNGAGACAGCTGTCACTGNCNAACTGTCTCTN
TAAANCAAANNCTCCGCNGGNGATGGGCTGAGCCAGTCCTAGNNGCTAGNTAGNGAT

FIG. 6A (cont.)

GNNGAGNTGTNGCACGNCGAGNGAGCATGNTCTGTACTGACTCATCAGGCGNCNACA
CGNTCTGTTCNAAAACATACCACACACACTCNCACCTNCGCAAAATTGCTCTNNAAAN
ATGCTTNTTTCACACNGNTNCAATCNCTATATNNTCTTCTATTCTNCNACGTNTNATTA
NNATCTTNCNCTGCANAACNATNCGNCCACCTNNANNACCTTANGCTTNGTTTCACGC
TTATAGCTCCCCTACACNTNNCAGCNNTTNCNNGTGAAGGGCCNCCCGAATCTACGA
NCATACTCTCTCCGTATATNGCCTCGGTCANCGCCATCTGCTGTNTNCTCNTCNCTNG
CNNTTNANCNGTNCGCTATCTCTNNNCCGGATCCNCNCCATATNNTNNCTCTACTTAN
AGCGTAANNTNTNCNCNCACTANTCACAACTTNTNCNTNNAACTCTATCTNCTCCTCT
CTACCACCTCACTTACTACCTNTTCACNCANTCTCCTTCNCTNTCCACTGATCTCCACA
TAGCTGCTNTACTCGCCANTTTATCATATNCACACNCTCTACGCTNNNTNT

Ref 2.1
Sequence of BAC4 using primer HC2S1, which spans nucleotides 1107-1126 of the cDNA. Exon sequence is underlined and represents nucleotides 1079-1097.

<u>CTTGTATTNAAAGAGGGTC</u>TGCAGGAAGAAGTGTGTAGTCATAAATACCTCACTGGA
TATTTTATACAGGATTCTAAAAAACCTATTAGCAATAGTATGCTAGAAATAGTCATTA
GCTTCTTGACCTTCTTAGAACTGCACACTCTATTGCACTGTACAGATTTCAGGATGGC
TGCAGGGATTGATTTGAAAACTAAGGACACATTTCAATAAACAATGTCTTCAATTGAT
TTTTAGGGCTCCTCCTACTTCAATGAAGGACTTCAGGTAGCTTATAATTACAGACACA
GGCTCAATACAATAAAAAAATTAGTAAGGCAGAGCTTTAAAAAAAAAAAAAGGAAAAA
GATAATTCTACCAGAGAAAGGCTACATGGTGACTTCTGTTACCAGTAACAACCCCCG
CACTACCTTTGGGTCTCCAGGAGCAAAACAGCTAATGTAGTTGTTGATCTGCTTGAAG
ACAAAGCCCCTGTCCATGAAGGTGAAACATCTCTGTGGAGGAAAACAAGCAAAAAAG
TTATTTCAGGTCCAAACATTTCGGAAATTTGGATTCAAAGCAGGCATTTATTGCTAAT
AAGTTTATCCACTGACATAAAAAACATGCCTTCAACATTGCCAGAGCACCTACTCTAT
TNTAGTCNCN

Ref 3.1
Sequence of BAC4 using primer C96AS, which spans nucleotides 1443-1452 of the cDNA. Exon sequence is underlined and represents nucleotides 1370-1422.

<u>AATCAGCAGACCAAACAGAGGCAGGTAGAGGGTGGCTATCCTTGCCTGATGGCTC</u>TG
AAAAGAAGACACACATGGTAAGTTTGACCCAGGATTCTGAGAACCGAACTAAGTTGG
TGCTGACCATCTCCTTTATTTGGATCCTTCCTATAAAGACAGATATTTGATTTTAGTCC
CAAAATAGAGCAAAATCTTAGTGCTGTTACCATGAATTTTCTAACTGATTACTTTCTTT
ACACCACTTAAAATAAAGGACATTATCAATGCACATTCCTTCCATTGGGGACCACTCA
CCCTTGAAGCATATCTGTCATCAAAAGAATGCTTTATCAGCAGGTTCTTGAGCACACT
GATGGCGATCAGACGGACCTCCCGGAACTCCTGGAGGGCTGTCCCCACCTCCCTNAG
TAACAGTCCCACCAAGAAGTGGTTTCTGCAGAACTCATCTGTTAATGAGTAGTCAAGC
TGGGAGGTCTGAAATGAGGATAGAAACTACTTTGNGTTAGGAAAGATGCAATGCTCT
TTTGAATAAAACAAACAAACCAAACNAACAAAAAAAAAAACTAAGACCCATCCTTNTGN
ATTTCAAGCCCACCCTGGGGTNGGTCAAAGAGATGATCAGNANTTTGGCNTTNAAAT
GAAGAAAGAAATNAATTNTCCAGGGGNTGTTCTNCTTTTTAGCACANGGAGGGATNT
TAANTGAAAACCAATTTAAATCCAATTNAGGNG

FIG. 6A (cont.)

Ref 4.1
Sequence of BAC4 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCCTTTCTGCAAGGCTGTTCCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAGC
ATTTCTCACACTGTTGATGTTTGGAGTTGAGGTTGTATATGGAGAAGCTAAATGGAAA
TCAAGCCAACAATAAAGTTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACTT
TAAGGGAAATTGCTTTTATTGCACTTATTTTTTCTGTTAGGAAGTTGGCTCAAGAGTT
GCATTCCATTACTTCACCTTTAAAGAACCAGGTCATATACAATGAGATAAAAAGAAAC
TAGTCTGAAACATTCAGATGTAAACATCAATTCACTTGTTAGAAACCACCTTTGATCG
CTAAAGACTAAATGCATACCTGTTTCAGAATGTGATAGAATGAAGACTTAAAAAAATT
AAAAGATAAATCCACCTACAACTATCAAATCACAAAATTAAACCACACAACAAACTTG
TAGCATTCAAACTGGTAATAAACACTGAGGAGCCTACCCAACTCTGAGGGGTGTCAT
GGGGTATTTTAAATTTTCGAGGAGAACACAGTGATATGTGACCTCAGCCAGAAGCTG
CTGTTTNAGCAGCAGGTTGGTGCTATGCTCCTTTTTGAAGACATATTTGTGAAGCTGG
GTATTTTGGGGGGCCTGCTTATGATAAAANGGCAAGGTNTTCAATGNAGGGGN

Ref 4.2
Sequence of BAC26 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCCTTTCTGGAAGGCTGTTACCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAG
CATTTCTCACACTGTTGATGTTTGGAGTTGAGGTTGTATATGGAGAAGCTAAATGGAA
ATCAAGCCAACAATAAAGTTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACT
TTAAGGGAAATTGCTTTTATTGCACTTATTTTTTCTGTTAGGAAGTTGGCTCAAGAGT
TGCATTCCATTACTTCACCTTTAAAGAACCAGGTCATATACAATGAGATAAAAAGAAA
CTAGTCTGAAACATTCAGATGTAAACATCAATTCACTTGTTAGAAACCACCTTTGATC
GCTAAAGACTAAATGCATACCTGTTTCAGAATGTGATAGAATGAAGACTTAAAAAAAT
TAAAAGATAAATCCACCTACAACTATCAAATCACAAAATTAAACCNCACAACAAACTT
GTAGCATTCAAACTGGTAATAAAACACTGAGGAGCCTACCCAACTTTGAGGGGTGTC
AATGGGGTNTTTTTAAATTTTTCGNGGGANANCCCAGTGNTATGGTGACCTTCACCCA
AGAAGCTTGTTTGTTTNACCAAGCNAGGTTGNNCTNTGCTCCTTTTTAGAANACNNTA
TTTTNNNAAATNCTGGNTTTTTTNNGNGGCCCCCTNCNTTNNT

Ref 5.1
Sequence of BAC4 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1724-1736.

TTCCTGGATAAGGTAATTGCTTTTACCCAACACAAATGTTTCTTATAATCAATGGATT
TAGCCCAAAGTAAACGTACTTCATGTTCTAGTGCCTTTTAAGTGTGACCTTTTGTTTT
TTTCTAAACCACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTTAAGGTTGGGGCCC
ATTCCTTGAAGTGCTCTGATTCCTGTTTCCAGTACCTCAGATCCTGGGCAGGGTTTGC
AGTGGAGCGTCTTGAGTGAATGGCTCTGGTGGGTTGAACGGGGAGGGACTCAAAAT
GCTGCCCATCTCAATTTCCTGTAGTCTTTTTATTTATTTATTTATTTTTTGAGACAGAG
TCTCGCTCTGTCGCCCAGGCTGGAGTACAGCGGCACGATCTCAATTNACTGCAACCT
CCGCCTCC:TGGGTTCAAACGACTCCTCTGCCTCAGCCTCCCCAGCAGC:TGGGACCA
CAGGCACAAGCCACCACCGCCCGGCTAATTTTTTGTNTTTTTAGTA:GAGAT:GGGGTT
TCACCATATTTGGCCAGGCTGGGCTCAAACTCCTGACC:TCGTCATCCGCNCCCTCGG
NCTNCCAAAGTGCTTGGGATTNCAGGCNGTGAGCCCACTTACACCTNGGGCAATTCC
CTGTNAGTCTTTTTTACCAGAGACACCATCATTCAACACAGCTTTTCCACCCACAA

FIG. 6A (cont.)

Ref 5.2
Sequence of BAC26 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1712-1736.

TGAGAAGAGCAATTTCCTGGATAAGGTAATTGCTTTTACCCAACACAAATGTTTCTTA
TAATCAATGGATTTAGCCCAAAGTAAACGTACTTCATGTTCTAGTGCCTTTTAAGTGT
GACCTTTTGTTTTTTTCTAAACCACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTTA
AGGTTGGGGCCCATTCCTTGAAGTGCTCTGATTCCTGTTTCCAGTACCTCAGATCCTG
GGCAGGGTTTGCAGTGGAGCGTCTTGAGTGAATGGCTCTGGTGGGTTGAACGGGGA
GGGACTCAAAATGCTGCCCATCTCAATTTCCTGTAGTCTTTTTATTTATTTATTTATTT
TTTGAGACAGAGTCTCGCTCTGTCGCCCAGGCTGGAGTACAGCGGCACGATCTCAAT
TCACTGCAACCTCCGNCTCCCTGGGTTCAAACGACTCCTCTGNCTNAGNCTCCC:AGC
AGCCTGGGAACCACAGGCTCANGCCACCACGCCCGGCTAATTNTTGTAATTTTNAGT
AANAAATTGGGGGTTCTCACCATNTTGGCCCAAGNCTTGGGCCTAAAAACCTTNCTNA
CCNTCGNCATTCNCNCCCCNACCNTGGGCNCTNCTCAAANGNGCTTGGGGATTTANC
ANNGGCNTTAACCCCCCNTATCACCGTGGNCCTTAATTT

Ref 6.1
Sequence of BAC4 using primer C2S7, which spans nucleotides 1918-1937 of the cDNA. Exon sequence is not found within this sequence.Since the primer is directed against exon sequence we presume that sequence derived from C2S7 is intron sequence.

NAGNGNGGGTTTNAGNCGTTTGAAGCCTGNNACGNGGTGNGTGCTNGAACTCTGTGG
GCTTTCAGGTACTGGGGTATCTGGGAGCCTGCTGTTTGCATTGCTAGTGCATCAGAC
CAGGGCTTTTTCCTCCCTGTAGCTGCTACTTATACACATAGCTCTAACTGAGATGATT
CTCCAGACAACTGATGCAGAGCAGCAAAAGCTTCTGCCGTTCTCCCCTTCTAGGAGT
GTCTCCTTTCTTTGGAAAGAGATCATGAGGGGCTAGATTGTAATGAAGTGAGGCTCA
GTGCTTGAGCACATCCGGTAAAAGTTCCAATATATTGGTCATAAAGTTTCTCATTCTT
TATAGCAGTTAATTTCTCTGGCTCATGAGTTTTCTTAGTTTTAATCTGACTTTTAAATT
AATGTCTCCAGCACCAGTCATATCCCCAGGGCAAACTCAAAGGCATGAGAGGCCAGA
CTCGGGTCCTGGTCATAGCAACCCCTGTCTAGGGCCTTGGTCCCTGCCTCCGCTTGT
GTGCTGTGGCGCAGGTCCTATGGGCCCTTAGGAAACAGGACCACCCTGTCGCACCCC
CTACAGAGACCAGCCAAGTTTGACATTAGATCACCGTAGCAATGTNTGCAAATTCCA
GTTTCTTGCTAAAACAGGTTAAGCCTTGCAGCCACTTTATCTGTAACTGGCNGAGGTT
TTGACATAAAA

Ref 7.1
Sequence of BAC4 using primer C2S8, which spans nucleotides 2143-2162 of the cDNA. Exon sequence is underlined and represents nucleotides 2182-2219.

CTCTCGACACGCTGTTTCTATTAACATTGGCGTTTAAGGTTTGTATCAATTTGCTGTT
CGNGGTTCTAGTTTTACCTTTCACATTCATTCTGCTTGGTAAGCTCAGTGAGCACAAA
CTTACTATGTTGCATTTTTACTTCAGCAATTATTTTTGTCCCTGTAAGGAAACCATTAA
TCTTTAAATTCCTTTAATGAAATCATTCCACAGTGAATGGCTTGAATGCCCTGAAATA
AAATTTAACTGGTCAGTGTGTGCTGCGCGCTTGGGTATGGTGGAAACACGGTCTCTG
GAGGCAGTTAACTCTTGGCTCGAACCTTGAGGATGGTGAATATAGGCACCTAATCAG

FIG. 6A (cont.)

GCATTTCTGCCTTGAATATCTTTAAATATATCCAAATGTTATAGCGTTTAATTAGATTT
TTATGTAGAAAGGAGCAATAAACACAAGACACATGTTTTCAGTTTTTTATCTGTTACT
GCATTAAATGATAAAAACGTTTTGGAGATAGAAAATGAAAGGGGTTTTTTTTTTGTCT
TGTTTTAAAGTTTTAGCAAATAATATTCAAGTAGGTGGAGATGGACTCTTCACCACTC
TCCTGTTTTTAGGAACCCAATACTTTTTCATTCTTGCTAAATGATTACTTCCATTTCTA
GCATAGAAAAGGAGAAAATTGGAATGAGTGTTTATAT

Ref 8.1
Sequence of BAC4 using primer C2S9, which spans nucleotides 2992-3011 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence
CGCTTTNAAATNCCAGCCGCTACTGCGGGGCGNTNAATTCGAAACGTGTTGTTNTCT
GTGATGCCTGGCTCTGATTGTGTGGGATTGGTCATCAGTGGCGGTTGGCAGNTGGGG
TTCATGGAAGCGGCCATGGGGACTGATGGCAGGCCCTTGGATTGCCACCGCAGAGCC
TGGCAGTGTCTTTGGTCTGCATTCCTACCGGCGAAGTCTCATTTCACCTCACGTGTTA
TCTCTTGGAAAGCATTCCTTTAGCGGGCTGTGTCTACCCTTCCATCCTCTCGTCCAAA
CTCCCCCTCCTTCTCTGTTCTGTCTCCTTCCCATCCTCTTCTCCCCAGTTCTTCTTCCT
ATGTTCCTTCCTCAGTGGTTTCTCTTCCTCTGTTTGACTTTCCAAGGTCATTTTGACTG
TTCCTGCTCCCAACTACAAAGATACTAAAATCTCACCTAACCACTCTTCTTCTTTCTTA
ATGAAAGAATGTTTTCAGTCCATCCCAAATTTGTGTGGACTTCACAAACCTTCTCTAA
AATGGAGCCTTTTCTCTTCCTACTCTTGACTAGNTGGTAAACGCTCCATGTTCTTGGC
CAGAACTCCCTGGTGAGTAGCGTCACTCCCACTTTCCTGTGCAGAACCAAGCCTCCT
AGAAAACTCCTTTGCANCTGAGTGGGTTGGGACACGCCCTTTNTTTGGG

Ref 9.1
Sequence of BAC4 using primer C2AS10, which spans nucleotides 3276-3295 of the cDNA. Exon sequence is underlined and represents nucleotides 3147-3234.
<u>TTTANACCNATNTATCCGNGTCAGTTANAGGAGTCTCTGAGAAATTTCCGACAGCGGT
GTGAGTTTGGGTTCCTTGTAAATATACTCCTTTCCATCTTCATCTTCAAAGAATCCCT</u>
GTGACATAAAGCACAATTAGAGCTATCCCTGAACGTAAGCCCAGGGCTTACCACCTA
GGAAGCGTTCTTTTATTACAAGGGGGAAAAAAAGGAATGGGTCTAAAAATCCAGCTG
AAATGGGCTTTCTGAATGAGAAAGAAAATGCTAATAACATGAAGTCTAGGTGCAAAG
GTAAAGGAAAAACACAACATTGCAAACTTATTCAAGAATGCAGTCATTAAGTGTTGAG
TGAAATGAAAGATTTTGGATACAAGACTAAGCTGTCCCAGGGAAGTCTAATGGGAGT
CAAGCCTGTTTCACTTTCCCAAGAAGCAGAACTCACTANAAAATGATGAGCAGCCCA
CGACAGGCAGGCTCAGAAGTGGACATGCCTCCCTTCTCCTGATGGCTNCCATGCACA
CAGGATTTTATGGCATGAACTGAAGCGTTTGGGGGTCTGGAGTAAGTTTAGTAAAAG
TTAGGTAAAGCTTGTATAAATTGTATTTTTGCTTTACCCGATGAGAAAAAAAATATTN
AAGACCTGGTAGCTTCAATATTCAAGAAAAATATTTTTCATNTCACCCG

FIG. 6A (cont.)

Ref 10.1
Sequence of BAC4 using primer C2S11, which spans nucleotides 3167-3186 of the cDNA. Exon sequence is underlined and represents nucleotides 3231-3296.
NGNANGTGGAGCCNCGANCCAGGGACAATCTNAACCTNCTTAAACTGTACTCGGATN
AATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGCAAGGTATTGACCATGTT
TGGANAAGTTTCATAGCAATGTAATGTTGTGATNCGATTACATATNATATATTTTTAA
ATGTNTATAGAAAAAAACACANGAAAAATATTAAGGATTGTTGGCCCGTGAGTGGCA
GGTGTATNTTCTTNCTGATCCTTTAGNGCTTTCCATTACATGCNTGACATTAAAAAAA
NCTTTATCGCCTAATTTTTGAAACATCTAATTTTACAAAATAATTAACCGTNTGGCCAN
GNATATTNTCATTTTTAGGNCCAGCTATTTAGAAACTCTGACANAAATGAGGGGCTGT
GGCTTNCCTNCCTNNACTTGNCCCTCTTTCNNGNATGTACCACATGAACTTGNCNCCT
CTTTCNNCTNACCGGGTGGCATGTTANAGGACAGGTTGAAACCNCANTNGGGCNGGA
NTTNGGTNNAATTGGGACACAATGGTACNANGCTCTATNGGAATNGAAACTCTCCCN
ACNNNCNGTGNNCCNTGGGGAAAATGNGNCNNATTCATTTTN

Ref 11.1
Sequence of BAC4 using primer C2S12, which spans nucleotides 3474-3493 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence
AGNANNGTTNNGCAGCTGCANNTCTGGACCCANAGGCCGCANGGGCACGAGCCNGG
ACACGCTCGGCAAAGAGCTGTCCAGAGGGATTCAGAAGCTTCAGGACTGGAAGGGTC
TTTCGAGCTCAGTTAGCCACCCCCACACCCATTTCAGTTTCACATTTATCTAGTGCTT
CCTTTTGAATACTTGGGATGTTTTTCTGTTGATCTGTTGGCACTTCCTTCTTCCACAA
GACCAGAAGCTCATATCCAATCTAAGGTCACTTACCCTTCTGAGAATCTGATGAAAAT
GGCGTGCCTTATGTGCCTAGATGCTTTTGCACACAGTCTAAGGTGACTTATGGACTCC
AGGTCCAGCAGCCACACCCAGTCCTGGGTCTCCGCACAGGGAGGGACCCGTCTTCAC
ACACCTGTCTCAGGTTCTAGCATTGGGCTGCTTCAGCGGTCTCAGGCTGTGAGTAAA
TGGGATGTGAGCTTGGATCGCCCCACGCTGTTGNCCCCCGGGGGGCTTGGCCAGCTG
GCCACTTNGAAATGCCTCCTTTTGCCCAGGAAAGCTCACTGCATTTCAATGGGGNTTN
TCCACGAAGTTCANCTTTANGGG

Ref 12.1
Sequence of BAC4 using primer C2S13, which spans nucleotides 3645-3664 of the cDNA. Exon sequence is underlined and represents nucleotides 3683-3699.
AGNAAGGTNNCTCANTNAANNCAGCGTGAGNGTTCAGGTGAGCCAGGCACAGCAGGC
CGGAGGGCAGCAGGGGACGTCCTTGCCCCTGGGTGACTTGAGAGTCGTTTCCACTAA
CAAGGTCTACTTGAGAGCCTCGGTTTACCAAGTGATCCCTGCTCCCTTCCCCCAACGT
NTGTGACATTTCTCCTGATATCAGAGGGGGAGGAAACCTCATGATCCCTGCCCCCCG
CCCCATGAGGACTGACTGTGGGGACAAAGAGCCAGATCTCATAGACTACCCTGATTT
GTCAGTATTTGGGGAATTCTGGGTGCCTGATTAGAAGCATCAAGACTCTTCTAAATNC
AAAGAAGTGTGGAGAGCAGTAGATTTTCCTATAAAACTGGTGTTGCTGGTTTCTATGA
AAATTGGATCCAAAAAAAGTCCTTAAGTTTACCCTCTTAATGGNATCTTTTGATTAAT
GGAATTCATTATTTTAATATAGCCCAATCAATCCAATTTTTCTTTATTGGTAGCATTTT
TATGTTCTCTTTAAAAAAATCTTGGNCTACCTCCAAAATTTCACAGATGTTCTCCTAG
GGTTTTCCTCCTTTTGGTTCAAGCATCCCATTCAANGTCTTGCAGTCCATTCTGGGG

FIG. 6A (cont.)

Ref 13.1
Sequence of BAC4 using primer C2S14, which spans nucleotides 4289-4308 of the cDNA. Exon sequence is underlined and represents nucleotides 4321-4448.

GACTTANATTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATGGCCTACAGAAAAAA
AAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGATGCCTGGGGGAC
CTTTTGCCTCGAGGCTGAGCTGGAAAATCTTGAAAATATTTTTTTTTTCCTGTGGCAC
ATTCAGGTTGAATACAAGAACTATTTTTGTGACTATGTTTTTGATGACCTAAGGGAAC
TGACCATTGTAATTTTTGTACCANTGAACCANGAGATTTAAGTGCTTTTATATTCATTT
CCTTGCATTTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAAACTAGTCAA
GCANTTTAGAACCAAAGGCCTATNTTNATAACCGCAACTATGCTNAAAAGNACAAAGT
AGTACAGNATATTGNTATGTACATATCATTTGGTAATACACNCCNGGCNTTCTGTACA
TATATGTATTACATTTCTACNTTTTTAATACTCCCNTGGGCTTATGCCNTTAAGGTTAA
NTTGNGATAAATTTNGGCTGTTCCNGTNTATNCNATACNCTTTT

Ref 14.1
Sequence of BAC4 using primer C2AS15, which spans nucleotides 4680-4700 of the cDNA. Exon sequence is underlined and represents nucleotides 4660-4683.

ATGAGAATGTAATACATATATGTACAGAATGCCAGGACTGTATTAACAATGATATGTA
CATAACAATATACTGTACTACTTTGTACTTTTCAGCATAGTTGCGGTTATTAATATAG
GCCTTTGGTTCTAAACTGCTTGACTAGTTTTAAGCTCACATAATTCCTTAAGCTTTCAT
ATTTTCTTAAATGCAAGGAAATGAATATAAAAGCACTAAATCTCCTGGTTCACTGGTA
CAAAAATTACAATGGTCAGTTCCCTTAGGTCATCAAAAACTAGTCACAAAAATAGTTC
TTGTATTCAACCTGAATGTGCCACAGGAAAAAAAAAATATTTTCAAGATTTTCCAGCT
CAGCCTCGAGGCAAAAGGCCCCCAGGCATCAATGTCAGNGCAGCCCTCCTGCCATGT
AGATCCCAGAACCTTTTTTTTCTGTAGGCCATCTATTCTAACACTACTCTGCAGGGAG
AATAAAATCTAAAGNCCAGCTCAAGAGTGCTACCACACCTTTGTTAAGACACAATGAA
AACTTTGGATATTGGCAGGNGAGATTTAAAAAAAAATGTGCCCTTTCTTACCACTCCT
ATAGNAAAGTCTGGTTAAGAAATAACCGTTGGTCTTTATTTTCCTTTTNTTTCCCCTTC
CCTTGGGNCTTCCTGGGGCTCGG

FIG. 6A (cont.)

```
HC2A    ------------------------------------------------------------
KIAA    ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ------------------------------------------------------------
HC5     ------------------------------------------------------------

HC2A    ------------------------------------------------------------
KIAA    FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ------------------------------------------------------------
HC5     ------------------------------------------------------------

HC2A    ---------------------------------------------VLHHHQNPEFYDEIK
KIAA    KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ------------------------------------------------------------
HC5     ------------------------------------------------------------

HC2A    IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA    IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ------------------------------------------------------------
HC5     ------------------------------------------------------------

HC2A    PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA    PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ----------------------------------------GPGPARSTVSISLISNSARV
HC5     ------------------------------------------------------------

HC2A    QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA    QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat     ------------------------------------------------------------
HC4     ----------------------MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1     --------------------------MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3     NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5     ------------------------------------------------------------
```

FIG. 6B

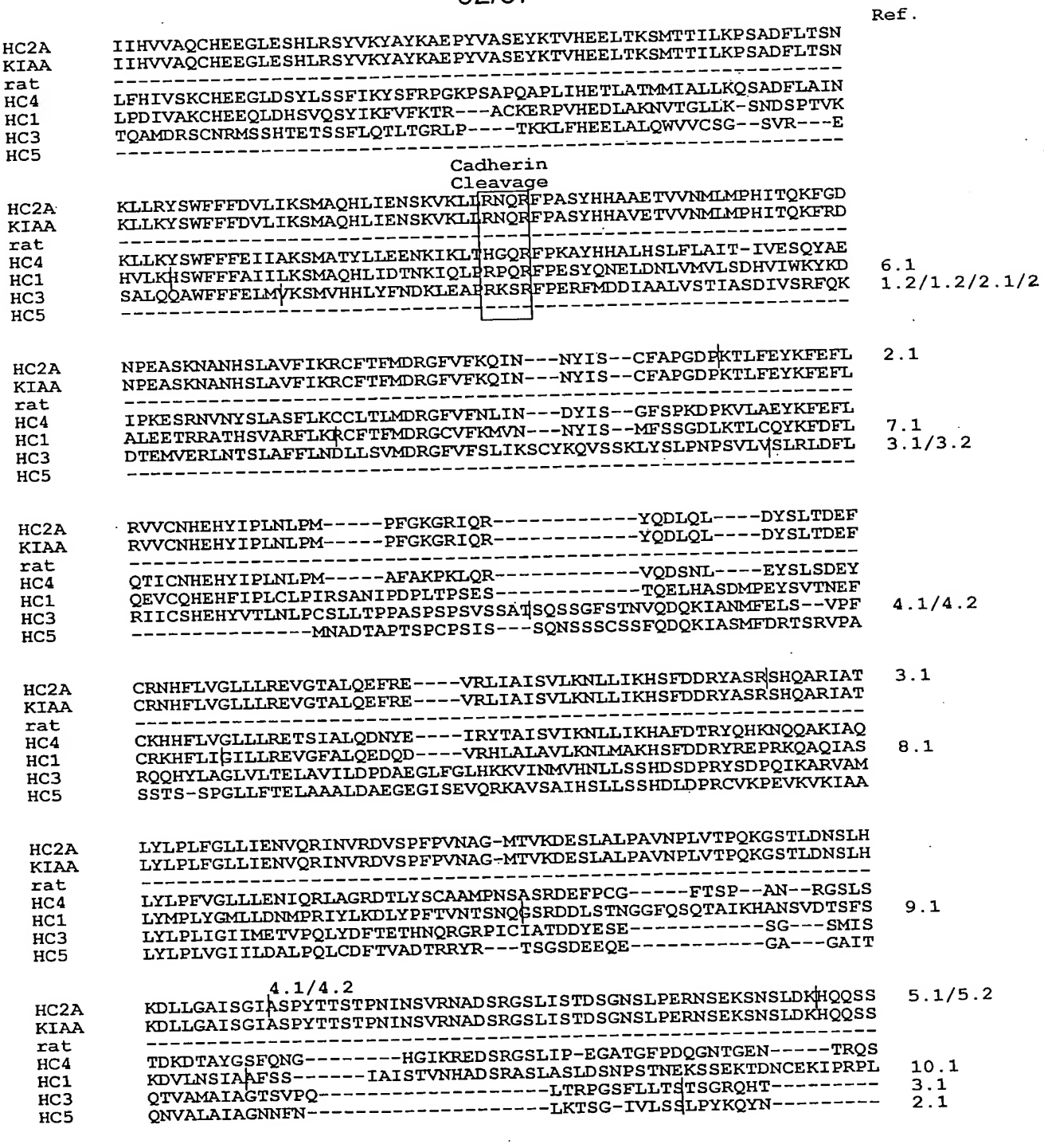

Ref.
HC2A IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
KIAA IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
rat ----------
HC4 LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1 LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVHEDLAKNVTGLLK-SNDSPTVK
HC3 TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E
HC5 ----------
Cadherin
Cleavage
HC2A KLLRYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAAETVVNMLMPHITQKFGD
KIAA KLLKYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAVETVVNMLMPHITQKFRD
rat ----------
HC4 KLLKYSWFFFEIIAKSMATYLLEENKIKLTHGQRFPKAYHHALHSLFLAIT-IVESQYAE
HC1 HVLKHSWFFFAIILKSMAQHLIDTNKIQLPRPQRFPESYQNELDNLVMVLSDHVIWKYKD 6.1
HC3 SALQQAWFFFELMVKSMVHHLYFNDKLEAPRKSRFPERFMDDIAALVSTIASDIVSRFQK 1.2/1.2/2.1/2
HC5 ----------
HC2A NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL 2.1
KIAA NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat ----------
HC4 IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1 ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLCQYKFDFL 7.1
HC3 DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFL 3.1/3.2
HC5 ----------
HC2A RVVCNHEHYIPLNLPM-----PFGKGRIQR----------YQDLQL----DYSLTDEF
KIAA RVVCNHEHYIPLNLPM-----PFGKGRIQR----------YQDLQL----DYSLTDEF
rat ----------
HC4 QTICNHEHYIPLNLPM-----AFAKPKLQR----------VQDSNL----EYSLSDEY
HC1 QEVCQHEHFIPLCLPIRSANIPDPLTPSES----------TQELHASDMPEYSVTNEF
HC3 RIICSHEHYVTLNLPCSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF 4.1/4.2
HC5 ----------MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA
HC2A CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT 3.1
KIAA CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat ----------
HC4 CKHHFLVGLLLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAKIAQ
HC1 CRKHFLIGILLREVGFALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS 8.1
HC3 RQQHYLAGLVLTELAVILDPDAEGLFGLHKKVINMVHNLLSSHDSDPRYSDPQIKARVAM
HC5 SSTS-SPGLLFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAA
HC2A LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat ----------
HC4 LYLPFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1 LYMPLYGMLLDNMPRIYLKDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFS 9.1
HC3 LYLPLIGIIMETVPQLYDFTETHNQRGRPICIATDDYESE----------SG---SMIS
HC5 LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE----------GA---GAIT
4.1/4.2
HC2A KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS 5.1/5.2
KIAA KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS
rat ----------
HC4 TDKDTAYGSFQNG--------HGIKREDSRGSLIP-EGATGFPDQGNTGEN-----TRQS
HC1 KDVLNSIAAFSS------IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL 10.1
HC3 QTVAMAIAGTSVPQ----------LTRPGSFLLTSTSGRQHT--------- 3.1
HC5 QNVALAIAGNNFN----------LKTSG-IVLSSLPYKQYN--------- 2.1

FIG. 6B (cont.)

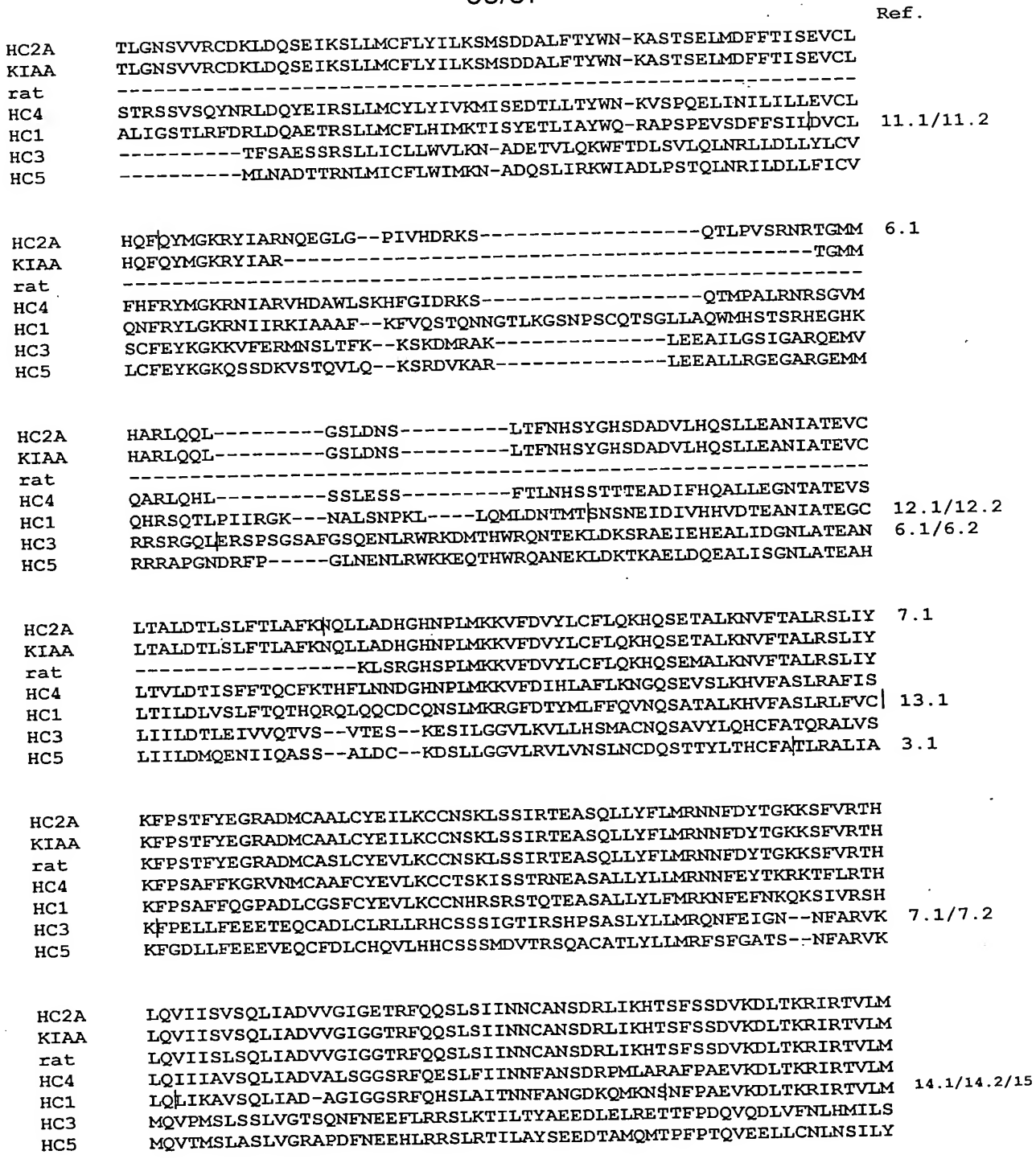

Ref.
HC2A TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
KIAA TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
rat ----------
HC4 STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLLTYWN-KVSPQELINILILLEVCL
HC1 ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSIIDVCL 11.1/11.2
HC3 ----------TFSAESSRSLLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLLDLLLYLCV
HC5 ----------MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV
HC2A HQFQYMGKRYIARNQEGLG--PIVHDRKS----------QTLPVSRNRTGMM 6.1
KIAA HQFQYMGKRYIAR----------TGMM
rat ----------
HC4 FHFRYMGKRNIARVHDAWLSKHFGIDRKS----------QTMPALRNRSGVM
HC1 QNFRYLGKRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK
HC3 SCFEYKGKKVFERMNSLTFK--KSKDMRAK----------LEEAILGSIGARQEMV
HC5 LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR----------LEEALLRGEGARGEMM
HC2A HARLQQL---------GSLDNS---------LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA HARLQQL---------GSLDNS---------LTFNHSYGHSDADVLHQSLLEANIATEVC
rat ----------
HC4 QARLQHL---------SSLESS---------FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1 QHRSQTLPIIRGK---NALSNPKL----LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC 12.1/12.2
HC3 RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTEKLDKSRAEIEHEALIDGNLATEAN 6.1/6.2
HC5 RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH
HC2A LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY 7.1
KIAA LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
rat ----------KLSRGHSPLMKKVFDVYLCFLQKHQSEMALKNVFTALRSLIY
HC4 LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1 LTILDLVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNQSATALKHVFASLRLFVC 13.1
HC3 LIILDTLEIVVQTVS--VTES--KESILGGVLKVLLHSMACNQSAVYLQHCFATQRALVS
HC5 LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDQSTTYLTHCFATLRALIA 3.1
HC2A KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
KIAA KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
rat KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC4 KFPSAFFKGRVNMCAAFCYEVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1 KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3 KFPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK 7.1/7.2
HC5 KFGDLLFEEEVEQCFDLCHQVLHHCSSSMDVTRSQACATLYLLMRFSFGATS--NFARVK
HC2A LQVIISVSQLIADVVGIGETRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
KIAA LQVIISVSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
rat LQVIISLSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
HC4 LQIIIAVSQLIADVALSGGSRFQESLFIINNFANSDRPMLARAFPAEVKDLTKRIRTVLM
HC1 LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM 14.1/14.2/15
HC3 MQVPMSLSSLVGTSQNFNEEFLRRSLKTILTYAEEDLELRETTFPDQVQDLVFNLHMILS
HC5 MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTPFPTQVEELLCNLNSILY

FIG. 6B (cont.)

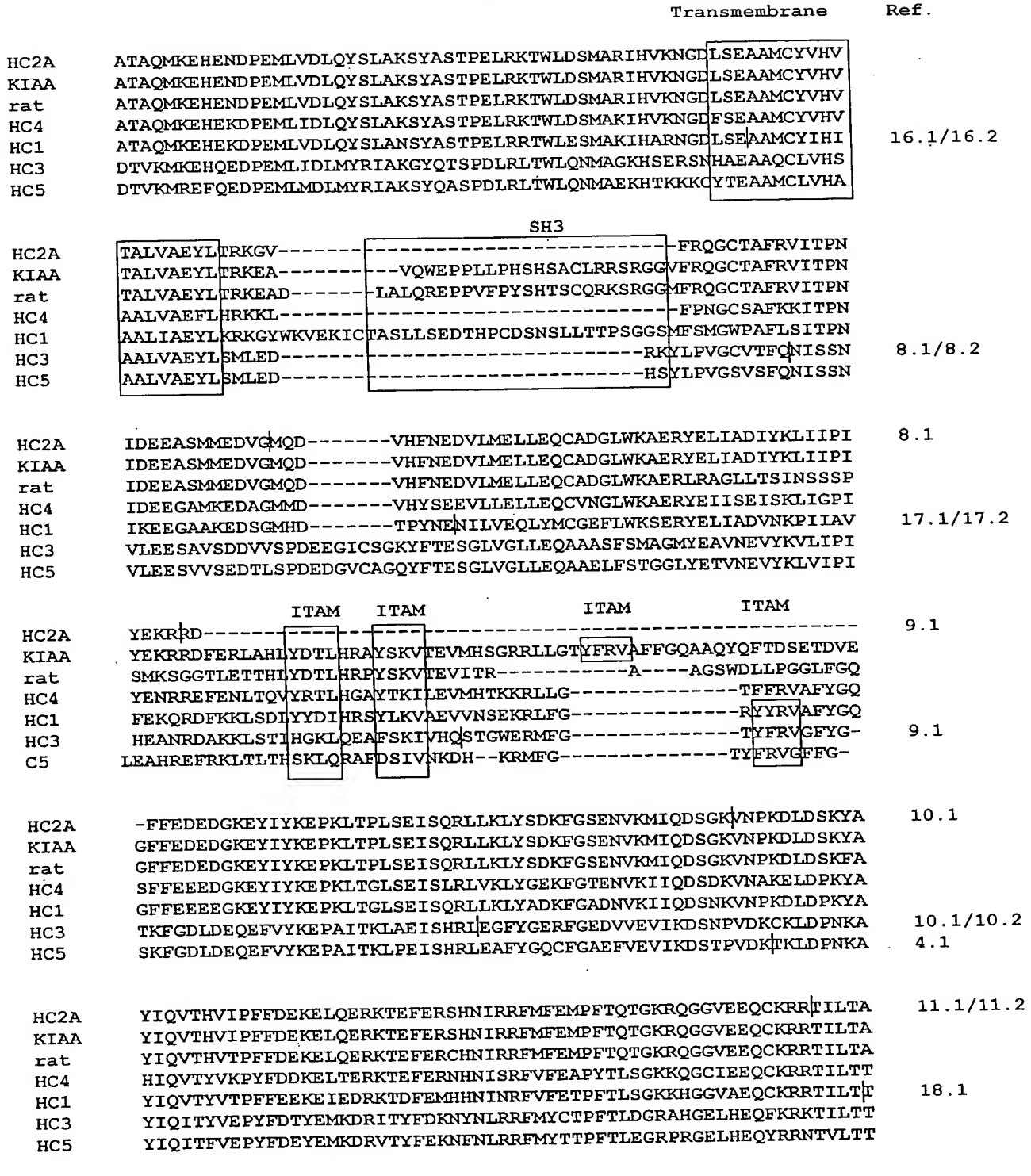

Transmembrane
Ref.
HC2A ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
KIAA ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
rat ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
HC4 ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLDSMAKIHVKNGDFSEAAMCYVHV
HC1 ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHI
HC3 DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPDLRLTWLQNMAGKHSERSNHAEAAQCLVHS
HC5 DTVKMREFQEDPEMLMDLMYRIAKSYQASPDLRLTWLQNMAEKHTKKKQYTEAAMCLVHA
16.1/16.2
SH3
HC2A TALVAEYLTRKGV----------FRQGCTAFRVITPN
KIAA TALVAEYLTRKEA----------VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat TALVAEYLTRKEAD---------LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4 AALVAEFLHRKKL----------FPNGCSAFKKITPN
HC1 AALIAEYLKRKGYWKVEKICTASLLSEDTHPCDSNSLLTTPSGGSMFSMGWPAFLSITPN
HC3 AALVAEYLSMLED----------RKYLPVGCVTFQNISSN
HC5 AALVAEYLSMLED----------HSYLPVGSVSFQNISSN
8.1/8.2
HC2A IDEEASMMEDVGMQD--------VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIPI
KIAA IDEEASMMEDVGMQD--------VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIPI
rat IDEEASMMEDVGMQD--------VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4 IDEEGAMKEDAGMMD--------VHYSEEVLLELLEQCVNGLWKAERYEIISEISKLIGPI
HC1 IKEEGAAKEDSGMHD--------TPYNENILVEQLYMCGEFLWKSERYELIADVNKPIIAV
HC3 VLEESAVSDDVVSPDEEGICSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLIPI
HC5 VLEESVVSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIPI
8.1
ITAM
ITAM
ITAM
ITAM
HC2A YEKRRD----------
KIAA YEKRRDFERLAHLYDTLHRAYSKVTEVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVE
rat SMKSGGTLETTHLYDTLHRPYSKVTEVITR----------A----AGSWDLLPGGLFGQ
HC4 YENRREFENLTQVYRTLHGAYTKILEVMHTKKRLLG----------TFFRVAFYGQ
HC1 FEKQRDFKKLSDLYYDIHRSYLKVAEVVNSEKRLFG----------RYYRVAFYGQ
HC3 HEANRDAKKLSTIHGKLQEAFSKIVHQSTGWERMFG----------TYFRVGFYG-
C5 LEAHREFRKLTLTHSKLQRAFDSIVNKDH--KRMFG----------TYFRVGFFG-
9.1
9.1
HC2A -FFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
KIAA GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
rat GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA
HC4 SFFEEEDGKEYIYKEPKLTGLSEISLRLVKLYGEKFGTENVKIIQDSDKVNAKELDPKYA
HC1 GFFEEEEGKEYIYKEPKLTGLSEISQRLLKLYADKFGADNVKIIQDSNKVNPKDLDPKYA
HC3 TKFGDLDEQEFVYKEPAITKLAEISHRIEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA
HC5 SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGQCFGAEFVEVIKDSTPVDKTKLDPNKA
10.1
10.1/10.2
4.1
HC2A YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4 HIQVTYVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLSGKKQGCIEEQCKRRTILTT
HC1 YIQVTYVTPFFEEKEIEDRKTDFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILTT
HC3 YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGELHEQFKRKTILTT
HC5 YIQITFVEPYFDEYEMKDRVTYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTT
11.1/11.2
18.1

FIG. 6B (cont.)

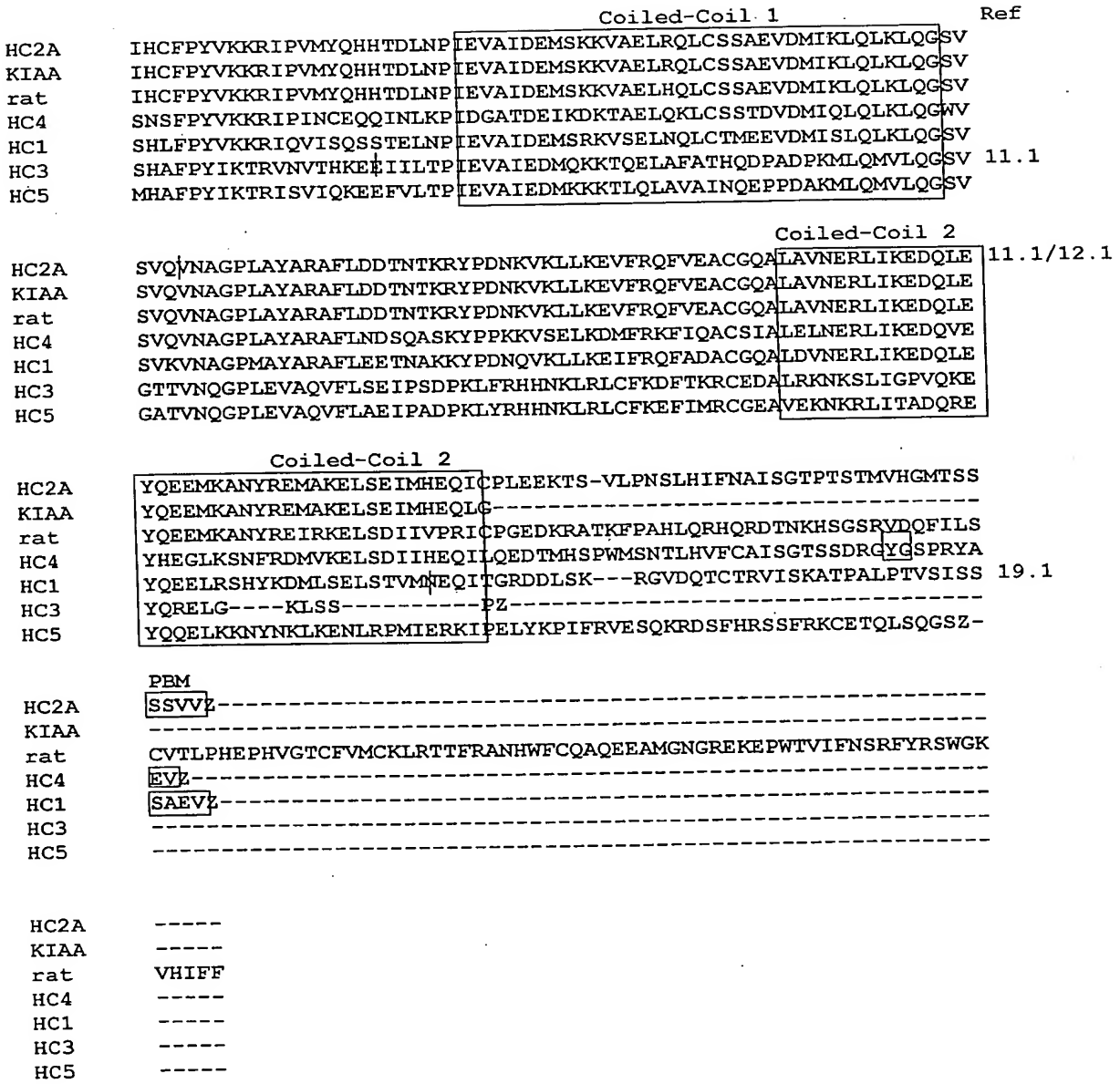

Coiled-Coil 1
Ref
HC2A IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV
HC4 SNSFPYVKKRIPINCEQQINLKPIDGATDEIKDKTAELQKLCSSTDVDMIQLQLKLQGWV
HC1 SHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3 SHAFPYIKTRVNVTHKEIIILTPIEVAIEDMQKKTQELAFATHQDPADPKMLQMVLQGSV 11.1
HC5 MHAFPYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPDAKMLQMVLQGSV
Coiled-Coil 2
HC2A SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE 11.1/12.1
KIAA SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
rat SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
HC4 SVQVNAGPLAYARAFLNDSQASKYPPKKVSELKDMFRKFIQACSIALELNERLIKEDQVE
HC1 SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE
HC3 GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE
HC5 GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE
Coiled-Coil 2
HC2A YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPTSTMVHGMTSS
KIAA YQEEMKANYREMAKELSEIMHEQLG----------
rat YQEEMKANYREIRKELSDIIVPRICPGEDKRATKFPAHLQRHQRDTNKHSGSRVDQFILS
HC4 YHEGLKSNFRDMVKELSDIIHEQILQEDTMHSPWMSNTLHVFCAISGTSSDRGYGSPRYA
HC1 YQEELRSHYKDMLSELSTVMNEQITGRDDLSK---RGVDQTCTRVISKATPALPTVSISS 19.1
HC3 YQRELG----KLSS----------PZ----------
HC5 YQQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGSZ-
PBM
HC2A SSVVZ----------
KIAA ----------
rat CVTLPHEPHVGTCFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGK
HC4 EVZ----------
HC1 SAEVZ----------
HC3 ----------
HC5 ----------
HC2A -----
KIAA -----
rat VHIFF
HC4 -----
HC1 -----
HC3 -----
HC5 -----

FIG. 6B (cont.)

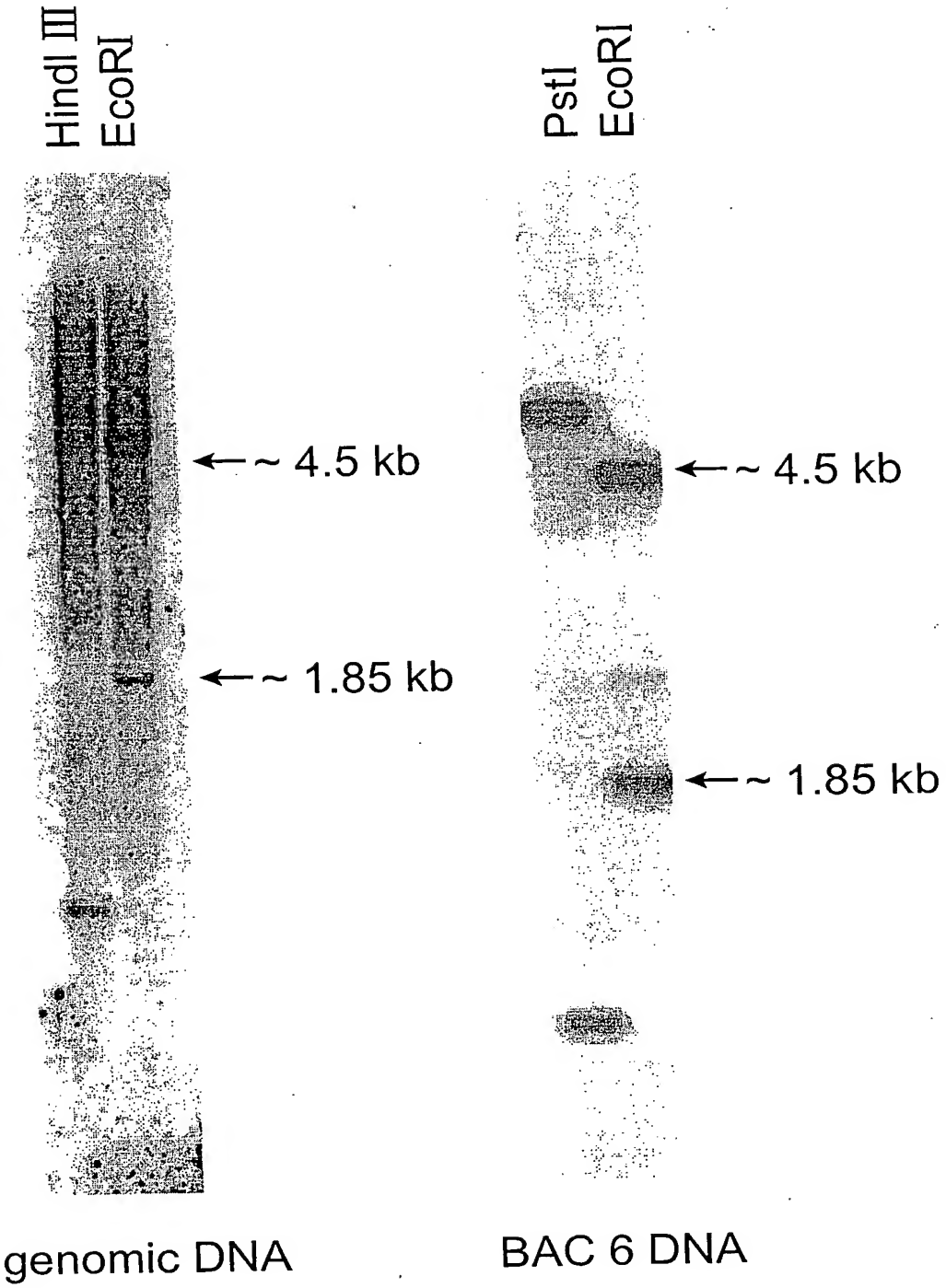

HindI III
EcoRI
~ 4.5 kb
~ 1.85 kb
genomic DNA
PstI
EcoRI
~ 4.5 kb
~ 1.85 kb
BAC 6 DNA

FIG. 7

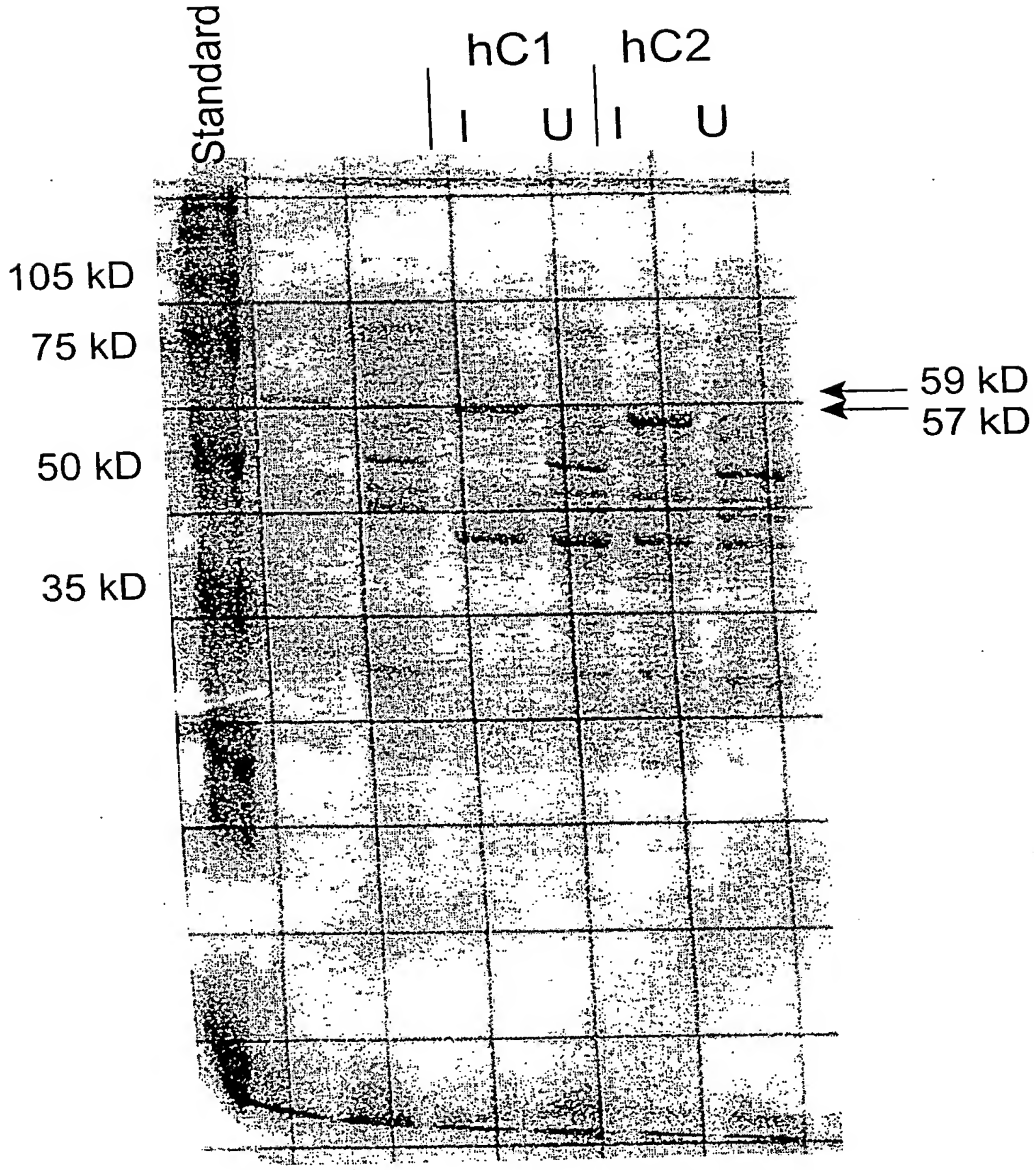


FIG. 8

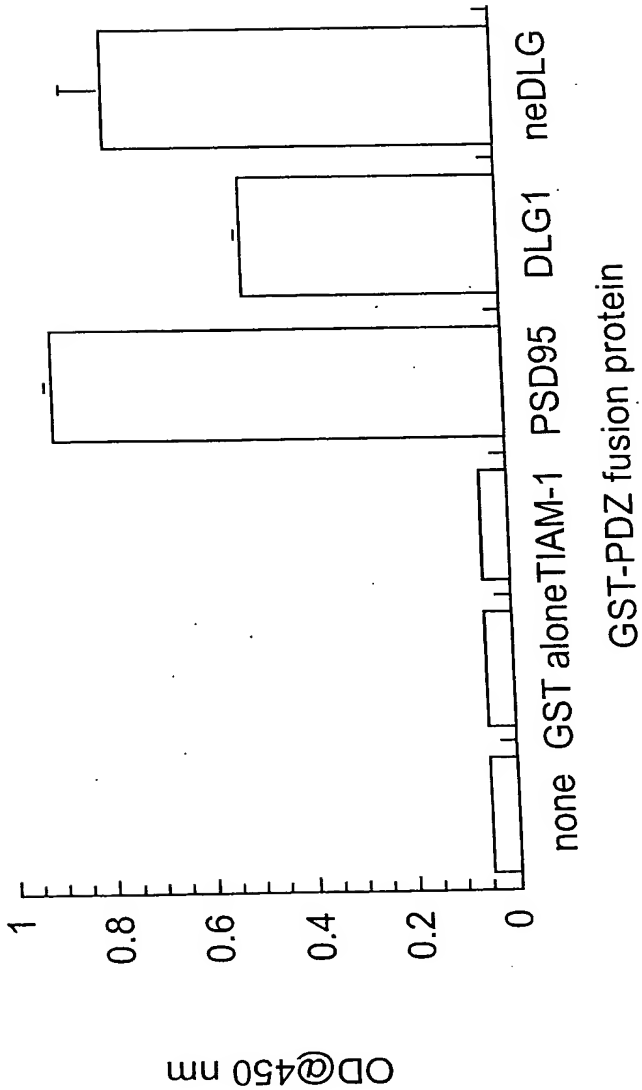

OD@450 nm
1
0.8
0.6
0.4
0.2
0
none
GST alone
TIAM-1
PSD95
DLG1
neDLG
GST-PDZ fusion protein

FIG. 9A

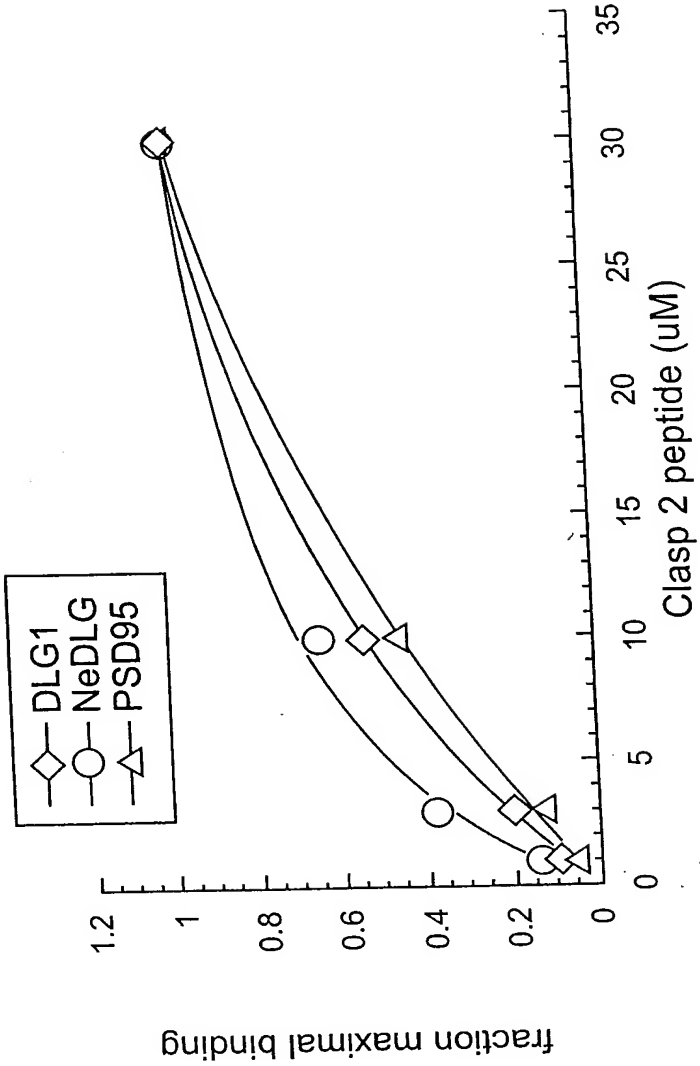

DLG1
NeDLG
PSD95
fraction maximal binding
1.2
1
0.8
0.6
0.4
0.2
0
0
5
10
15
20
25
30
35
Clasp 2 peptide (uM)

FIG. 9B

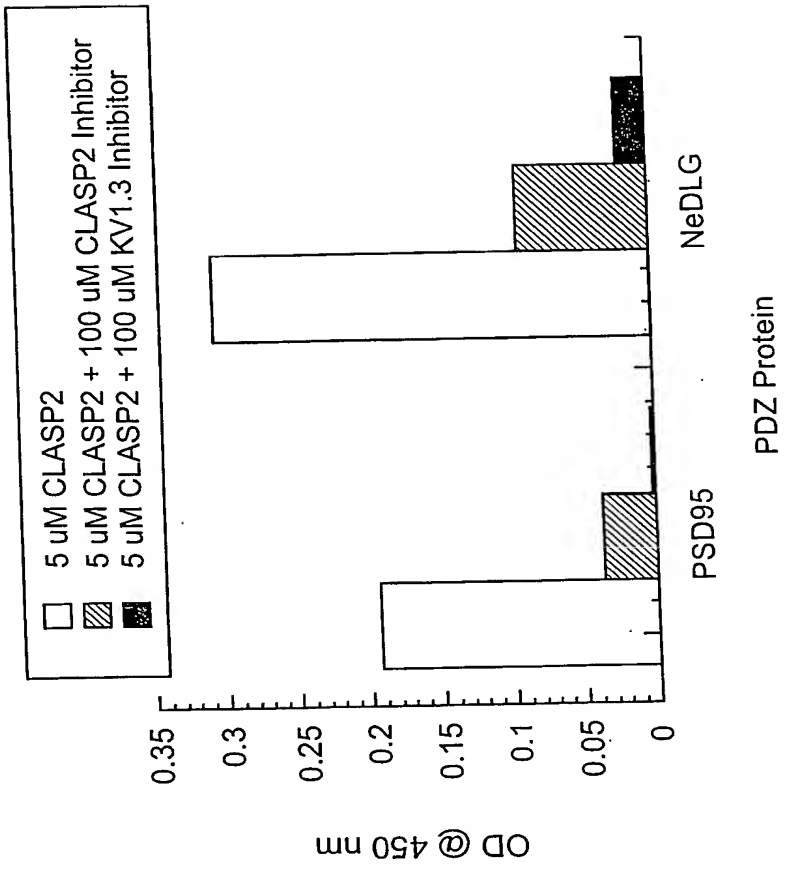

5 uM CLASP2
5 uM CLASP2 + 100 uM CLASP2 Inhibitor
5 uM CLASP2 + 100 uM KV1.3 Inhibitor
OD @ 450 nm
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
PSD95
NeDLG
PDZ Protein

FIG. 9C

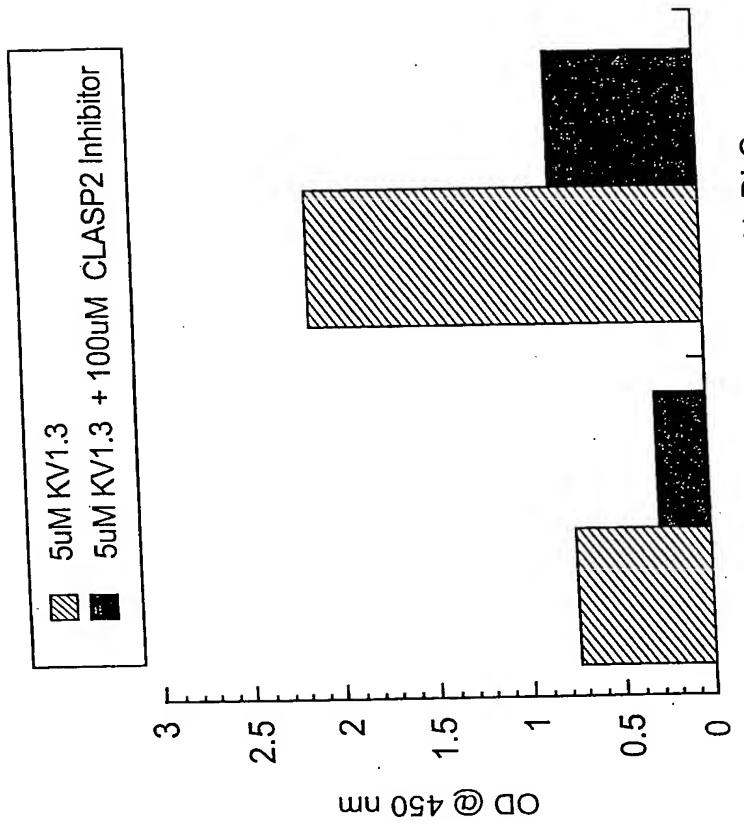

5uM KV1.3
5uM KV1.3 + 100uM CLASP2 Inhibitor
OD @ 450 nm
3
2.5
2
1.5
1
0.5
0
PSD95
NeDLG
PDZ Protein

FIG. 9D

```
    |  10      |  20      |  30      |  40      |  50      |  60      |  70      |  80
  1 AATTGTAATA CGACTCACTA TAGGGCGAAT TGGGTACCGG GCCCCCCCTC GAGGTCGACG GTATCGATAA GCTTGATATC 80
 81 GAATTCGGCA CGAGTTTTAC ACCATCACCA AAACCCAGAA TTTTATGATG AGATTAAAAT AGAGTTGCCC ACTCAGCTGC 160
161 ATGAAAAGCA CCACCTGTTG CTCACATTCT TCCATGTCAG CTGTGACAAC TCAAGTAAAG GAAGCACGAA GAAGAGGGAT 240
241 GTCGTTGAAA CCCAAGTTGG CTACTCCTGG CTTCCCCTCC TGAAAGACGG AAGGGTGGTG ACAAGCGAGC AGCACATCCC 320
321 GGTCTCGGCG AACCTTCCTT CGGGCTATCT TGGCTACCAA GAGCTTGGGA TGGGCAGGCA TTATGGTCCG GAAATTAAAT 400
401 GGGTAGATGG AGGCAAGCCA CTGCTGAAAA TTTCCACTCA TCTGGTTTCT ACAGGGATAC TCAGGATCAG CATTTACATA 480
481 ATTTTTTCCA GTACTGTCAG AAAACCGAAT CTGGAGCCCA AGCCTTAGGA AACGAACTTG TAAAGTACCT TAAGAGTCTG 560
561 CATGCGATGG AAGGCCACGT GATGATCGCC TTCTTGCCCA CTATCCTAAA CCAGCTGTTC CGAGTCCTCA CCAGAGCCAC 640
641 ACAGGAAGAA GTCGCGGTTA ACGTGACTCG GGTCATTATT CATGTGGTTG CCCAGTGCCA TGAGGAAGGA TTGGAGAGCC 720
721 ACTTGAGGTC ATATGTTAAG TACGCGTATA AGGCTGAGCC ATATGTTGCC TCTGAATACA AGACAGTGCA TGAAGAACTG 800
801 ACCAAATCCA TGACCACGAT TCTCAAGCCT TCTGCCGATT TCCTCACCAG CAACAAACTA CTGAGGTACT CATGGTTTTT 880
881 CTTTGATGTA CTGATCAAAT CTATGGCTCA GCATTTGATA GAGAACTCCA AAGTTAAGTT GCTGCGAAAC CAGAGATTTC 960
961 CTGCATCCTA TCATCATGCA GCGGAAACCG TTGTAAATAT GCTGATGCCA CACATCACTC AGAAGTTTGG AGATAATCCA 1040
1041 GAGGCATCTA AGAACGCGAA TCATAGCCTT GCTGTCTTCA TCAAGAGATG TTTCACCTTC ATGGACAGGG GCTTTGTCTT 1120
1121 CAAGCAGATC AACAACTACA TTAGCTGTTT TGCTCCTGGA GACCCAAAGA CCCTCTTTGA ATACAAGTTT GAATTTCTCC 1200
1201 GTGTAGTGTG CAACCATGAA CATTATATTC CGTTGAACTT ACCAATGCCA TTTGGAAAAG GCAGGATTCA AAGATACCAA 1280
1281 GACCTCCAGC TTGACTACTC ATTAACAGAT GAGTTCTGCA GAAACCACTT CTTGGTGGGA CTGTTACTGA GGGAGGTGGG 1360
1361 GACAGCCCTC CAGGAGTTCC GGGAGGTCCG TCTGATCGCC ATCAGTGTGC TCAAGAACCT GCTGATAAAG CATTCTTTTG 1440
1441 ATGACAGATA TGCTTCAAGG AGCCATCAGG CAAGGATAGC CACCCTCTAC CTGCCTCTGT TTGGTCTGCT GATTGAAAAC 1520
1521 GTCCAGCGGA TCAATGTGAG GGATGTGTCA CCCTTCCCTG TGAACGCGGG CATGACCGTG AAGGATGAAT CCCTGGCTCT 1600
1601 ACCAGCTGTG AATCCGCTGG TGACGCCGCA GAAGGGAAGC ACCCTGGACA ACAGCCTGCA CAAGGACCTG CTGGGCGCCA 1680
1681 TCTCCGGCAT TGCTTCTCCA TATACAACCT CAACTCCAAA CATCAACAGT GTGAGAAATG CTGATTCGAG AGGATCTCTC 1760
1761 ATAAGCACAG ATTCGGGTAA CAGCCTTCCA GAAAGGAATA GTGAGAAGAG CAATTCCCTG GATAAGCACC AACAAAGTAG 1840
1841 CACATTGGGA AATTCCGTGG TTCGCTGTGA TAAACTTGAC CAGTCTGAGA TTAAGAGCCT ACTGATGTGT TTCCTCTACA 1920
1921 TCTTAAAGAG CATGTCTGAT GATGCTTTGT TTACATATTG GAACAAGGCT TCAACATCTG AACTTATGGA TTTTTTTACA 2000
2001 ATATCTGAAG TCTGCCTGCA CCAGTTCCAG TACATGGGGA AGCGATACAT AGCCAGGAAC CAGGAGGGGT TGGGACCCAT 2080
2081 AGTTCATGAT CGAAAGTCTC AGACATTGCC TGTTTCCCGT AACAGAACAG GAATGATGCA TGCCAGATTG CAGCAGCTGG 2160
2161 GCAGCCTGGA TAACTCTCTC ACTTTTAACC ACAGCTATGG CCACTCGGAC GCAGATGTTC TGCACCAGTC ATTACTTGAA 2240
2241 GCCAACATTG CTACTGAGGT TTGCCTGACA GCTCTGGACA CGCTTTCTCT ATTTACATTG GCGTTTAAGA ACCAGCTCCT 2320
2321 GGCCGACCAT GGACATAATC CTCTCATGAA AAAAGTTTTT GATGTCTACC TGTGTTTTCT TCAAAAACAT CAGTCTGAAA 2400
2401 CGGCTTTAAA AAATGTCTTC ACTGCCTTAA GGTCCTTAAT TTATAAGTTT CCCTCAACAT TCTATGAAGG GAGAGCGGAC 2480
2481 ATGTGTGCGG CTCTGTGTTA CGAGATTCTC AAGTGCTGTA ACTCCAAGCT GAGCTCCATC AGGACGGAGG CCTCCCAGCT 2560
2561 GCTCTACTTC CTGATGAGGA ACAACTTTGA TTACACTGGA AAGAAGTCCT TTGTCCGGAC ACATTTGCAA GTCATCATAT 2640
2641 CTGTCAGCCA GCTGATAGCA GACGTTGTTG GCATTGGGGA AACCAGATTC CAGCAGTCCC TGTCCATCAT CAACAACTGT 2720
2721 GCCAACAGTG ACCGGCTTAT TAAGCACACC AGCTTCTCCT CTGATGTGAA GGACTTAACC AAAAGGATAC GCACGGTGCT 2800
2801 AATGGCCACC GCCCAGATGA AGGAGCATGA GAACGACCCA GAGATGCTGG TGGACCTCCA GTACAGCCTG GCCAAATCCT 2880
2881 ATGCCAGCAC GCCCGAGCTC AGGAAGACGT GGCTCGACAG CATGGCCAGG ATCCATGTCA AAAATGGCGA TCTCTCAGAG 2960
2961 GCAGCAATGT GCTATGTCCA CGTAACAGCC CTAGTGGCAG AATATCTCAC ACGGAAAGGC GTGTTTAGAC AAGGATGCAC 3040
3041 CGCCTTCAGG GTCATTACCC CAAACATCGA CGAGGAGGCC TCCATGATGG AAGACGTGGG GATGCAGGAT GTCCATTTCA 3120
3121 ACGAGGATGT GCTGATGGAG CTCCTTGAGC AGTGCGCAGA TGGACTCTGG AAAGCCGAGC GCTACGAGCT CATCGCCGAC 3200
3201 ATCTACAAAC TTATCATCCC CATTTATGAG AAGCGGAGGG ATTTCTTTGA AGATGAAGAT GGAAAGGAGT ATATTTACAA 3280
3281 GGAACCCAAA CTCACACCGC TGTCGGAAAT TTCTCAGAGA CTCCTTAAAC TGTACTCGGA TAAATTTGGT TCTGAAAATG 3360
3361 TCAAAATGAT ACAGGATTCT GGCAAGGTCA ACCCTAAGGA TCTGGATTCT AAGTATGCAT ACATCCAGGT GACTCACGTC 3440
3441 ATCCCCTTCT TTGACGAAAA AGAGTTGCAA GAAAGGAAAA CAGAGTTTGA GAGATCCCAC AACATCCGCC GCTTCATGTT 3520
3521 TGAGATGCCA TTTACGCAGA CCGGGAAGAG GCAGGGCGGG GTGGAAGAGC AGTGCAAACG GCGCACCATC CTGACAGCCA 3600
3601 TACACTGCTT CCCTTATGTG AAGAAGCGCA TCCCTGTCAT GTACCAGCAC CACACTGACC TGAACCCCAT CGAGGTGGCC 3680
3681 ATTGACGAGA TGAGTAAGAA GGTGGCGGAG CTCCGGCAGC TGTCGCTCCTC GGCCGAGGTG GACATGATCA AACTGCAGCT 3760
3761 CAAACTCCAG GGCAGCGTGA GTGTTCAGGT CAATGCTGGC CCACTAGCAT ATGCGCGAGC TTTCTTAGAT GATACAAACA 3840
3841 CAAAGCGATA TCCTGACAAT AAAGTGAAGC TGCTTAAGGA AGTTTTCAGG CAATTTGTGG AAGCTTGCGG TCAAGCCTTA 3920
3921 GCGGTAAACG AACGTCTGAT TAAAGAAGAC CAGCTCGAGT ATCAGGAAGA AATGAAAGCC AACTACAGGG AAATGGCGAA 4000
4001 GGAGCTTTCT GAAATCATGC ATGAGCAGAT CTGCCCCCTG GAGGAGAAGA CGAGCGTCTT ACCGAATTCC CTTCACATCT 4080
4081 TCAACGCCAT CAGTGGGACT CCAACAAGCA CAATGGTTCA CGGGATGACC AGCTCGTCTT CGGTCGTGTG ATTACATCTC 4160
4161 ATGGCCCGTG TGTGGGGACT TGCTTTGTCA TTTGCAAACT CAGGATGCTT TCCAAAGCCA ATCACTGGGG AGACCGAGCA 4240
4241 CAGGGAGGAC CAAGGGGAAG GGGAGAGAAA GGAAATAAAG AACAACGTTA TTTCTTAACA GACTTTCTAT AGGAGTTGTA 4320
4321 AGAAGGTGCA CATATTTTTT TAAATCTCAC TGGCAATATT CAAAGTTTTC ATTGTGTCTT AACAAAGGTG TGGTAGACAC 4400
4401 TCTTGAGCTG GACTTAGATT TTATTCTTCC TTGCAGAGTA GTGTTAGAAT AGATGGCCTA CAGAAAAAAA AGGTTCTGGG 4480
4481 ATCTACATGG CAGGGAGGGC TGCACTGACA TTGATGCCTG GGGGACCTTT TGCCTCGACT CGTGCCGGAA ATCTGATCGT 4560
4561 AATCAGGGTA CAGAACTTAC TAGTTTTGTC TAGGAGTATG TTGTATGACT AGGATTTGTG CTATTATCTC ATTCAACAAC 4640
4641 ATAGAGCAAG AATAGTGAGC TAACTGAGCT AGACACTCAA TTAATCCGCT ACTGGCTTCA AGTCAGAACT TTGTCATTAA 4720
4721 TCATCGACTC CGGGACGGTC ATATATGTAT TACATTTCTA CATTTTTAAT ACTCACATGG GCTTATGCAT TAAGTTTAAT 4800
4801 TGTGATAAAT TTGTGCTGGT CCAGTATATG CAATACACTT TAATGGTTTA TTCTTGTCAT AAAAATGTGC AATATGGAGA 4880
4881 TGTATACAAG TCTTTACT                                                                    4898
    |  10      |  20      |  30      |  40      |  50      |  60      |  70      |  80
```

FIG.10A

```
         |  10      |  20      |  30      |  40      |  50      |  60      |  70      |  80
   1 MEGHVMIAFL PTILNQLFRV LTRATQEEVA VNVTRVIIHV VAQCHEEGLE SHLRSYVKYA YKAEPYVASE YKTVHEELTK 80
  81 SMTTILKPSA DFLTSNKLLR YSWFFFDVLI KSMAQHLIEN SKVKLLRNQR FPASYHHAAE TVVNMLMPHI TQKFGDNPEA 160
 161 SKNANHSLAV FIKRCFTFMD RGFVFKQINN YISCFAPGDP KTLFEYKFEF LRVVCNHEHY IPLNLPMPFG KGRIQRYQDL 240
 241 QLDYSLTDEF CRNHFLVGLL LREVGTALQE FREVRLIAIS VLKNLLIKHS FDDRYASRSH QARIATLYLP LFGLLIENVQ 320
 321 RINVRDVSPF PVNAGMTVKD ESLALPAVNP LVTPQKGSTL DNSLHKDLLG AISGIASPYT TSTPNINSVR NADSRGSLIS 400
 401 TDSGNSLPER NSEKSNSLDK HQQSSTLGNS VVRCDKLDQS EIKSLLMCFL YILKSMSDDA LFTYWNKAST SELMDFFTIS 480
 481 EVCLHQFQYM GKRYIARNQE GLGPIVHDRK SQTLPVSRNR TGMMHARLQQ LGSLDNSLTF NHSYGHSDAD VLHQSLLEAN 560
 561 IATEVCLTAL DTLSLFTLAF KNQLLADHGH NPLMKKVFDV YLCFLQKHQS ETALKNVFTA LRSLIYKFPS TFYEGRADMC 640
 641 AALCYEILKC CNSKLSSIRT EASQLLYFLM RNNFDYTGKK SFVRTHLQVI ISVSQLIADV VGIGETRFQQ SLSIINNCAN 720
 721 SDRLIKHTSF SSDVKDLTKR IRTVLMATAQ MKEHENDPEM LVDLQYSLAK SYASTPELRK TWLDSMARIH VKNGDLSEAA 800
 801 MCYVHVTALV AEYLTRKGVF RQGCTAFRVI TPNIDEEASM MEDVGMQDVH FNEDVLMELL EQCADGLWKA ERYELIADIY 880
 881 KLIIPIYEKR RDFFEDEDGK EYIYKEPKLT PLSEISQRLL KLYSDKFGSE NVKMIQDSGK VNPKDLDSKY AYIQVTHVIP 960
 961 FFDEKELQER KTEFERSHNI RRFMFEMPFT QTGKRQGGVE EQCKRRTILT AIHCFPYVKK RIPVMYQHHT DLNPIEVAID 1040
1041 EMSKKVAELR QLCSSAEVDM IKLQLKLQGS VSVQVNAGPL AYARAFLDDT NTKRYPDNKV KLLKEVFRQF VEACGQALAV 1120
1121 NERLIKEDQL EYQEEMKANY REMAKELSEI MHEQICPLEE KTSVLPNSLH IFNAISGTPT STMVHGMTSS SSVV       1195
         |  10      |  20      |  30      |  40      |  50      |  60      |  70      |  80
```

FIG. 10A (cont.)

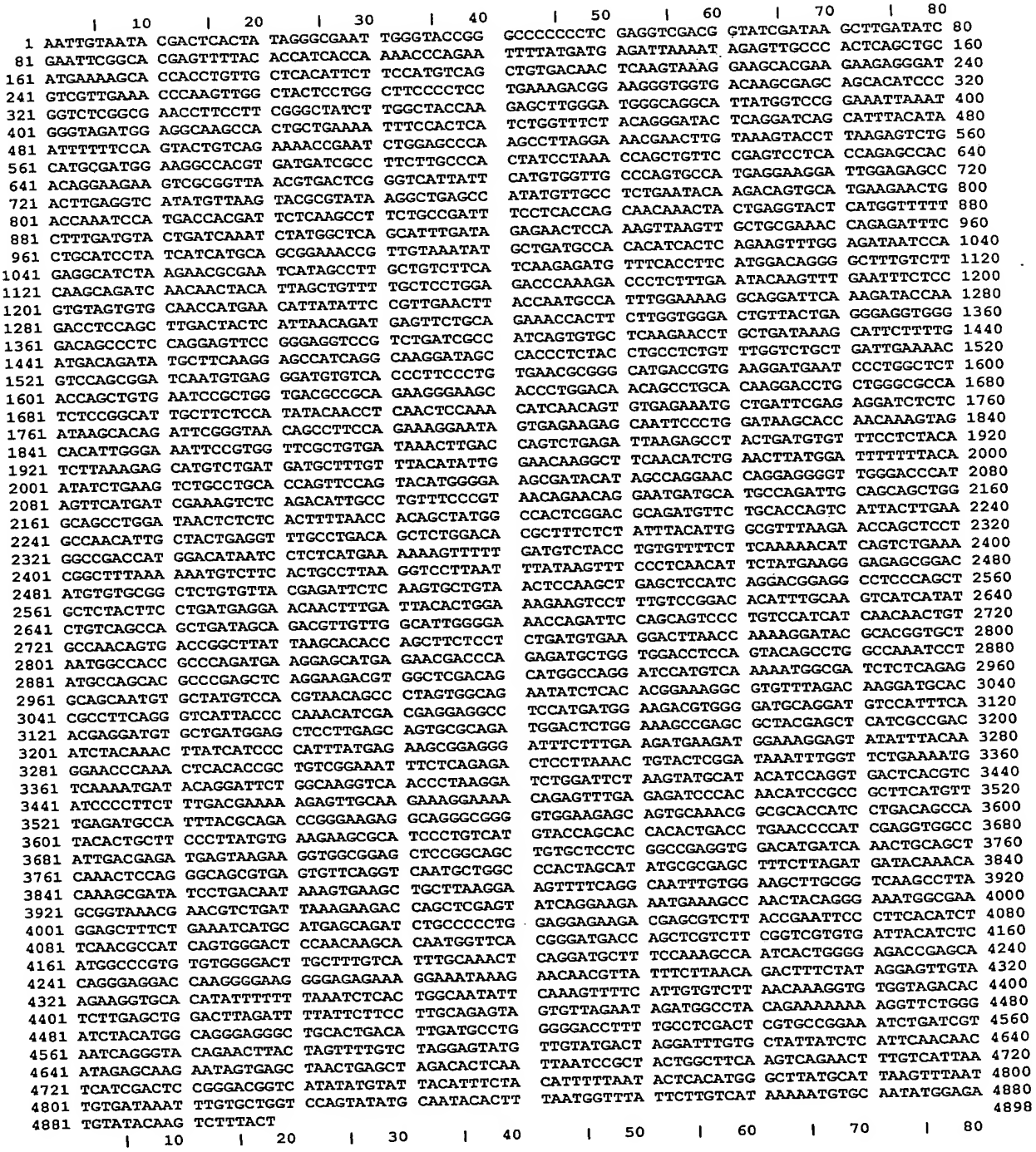


FIG.10B

```
        |   10      |   20      |   30      |   40      |   50      |   60      |   70      |   80
  1 MEGHVMIAFL PTILNQLFRV LTRATQEEVA VNVTRVIIHV  VAQCHEEGLE SHLRSYVKYA YKAEPYVASE YKTVHEELTK 80
 81 SMTTILKPSA DFLTSNKLLR YSWFFFDVLI KSMAQHLIEN  SKVKLLRNQR FPASYHHAAE TVVNMLMPHI TQKFGDNPEA 160
161 SKNANHSLAV FIKRCFTFMD RGFVFKQINN YISCFAPGDP  KTLFEYKFEF LRVVCNHEHY IPLNLPMPFG KGRIQRYQDL 240
241 QLDYSLTDEF CRNHFLVGLL LREVGTALQE FREVRLIAIS  VLKNLLIKHS FDDRYASRSH QARIATLYLP LFGLLIENVQ 320
321 RINVRDVSPF PVNAGMTVKD ESLALPAVNP LVTPQKGSTL  DNSLHKDLLG AISGIASPYT TSTPNINSVR NADSRGSLIS 400
401 TDSGNSLPER NSEKSNSLDK HQQSSTLGNS VVRCDKLDQS  EIKSLLMCFL YILKSMSDDA LFTYWNKAST SELMDFFTIS 480
481 EVCLHQFQYM GKRYIARNQE GLGPIVHDRK SQTLPVSRNR  TGMMHARLQQ LGSLDNSLTF NHSYGHSDAD VLHQSLLEAN 560
561 IATEVCLTAL DTLSLFTLAF KNQLLADHGH NPLMKKVFDV  YLCFLQKHQS ETALKNVFTA LRSLIYKFPS TFYEGRADMC 640
641 AALCYEILKC CNSKLSSIRT EASQLLYFLM RNNFDYTGKK  SFVRTHLQVI ISVSQLIADV VGIGETRFQQ SLSIINNCAN 720
721 SDRLIKHTSF SSDVKDLTKR IRTVLMATAQ MKEHENDPEM  LVDLQYSLAK SYASTPELRK TWLDSMARIH VKNGDLSEAA 800
801 MCYVHVTALV AEYLTRKGVF RQGCTAFRVI TPNIDEEASM  MEDVGMQDVH FNEDVLMELL EQCADGLWKA ERYELIADIY 880
881 KLIIPIYEKR RDFFEDEDGK EYIYKEPKLT PLSEISQRLL  KLYSDKFGSE NVKMIQDSGK VNPKDLDSKY AYIQVTHVIP 960
961 FFDEKELQER KTEFERSHNI RRFMFEMPFT QTGKRQGGVE  EQCKRRTILT AIHCFPYVKK RIPVMYQHHT DLNPIEVAID 1040
1041 EMSKKVAELR QLCSSAEVDM IKLQLKLQGS VSVQVNAGPL  AYARAFLDDT NTKRYPDNKV KLLKEVFRQF VEACGQALAV 1120
1121 NERLIKEDQL EYQEEMKANY REMAKELSEI MHEQICPLEE  KTSVLPNSLH IFNAISGTPT STMVHGMTSS SSVV       1195
        |   10      |   20      |   30      |   40      |   50      |   60      |   70      |   80
```

FIG. 10B (cont.)

```
          |  10       |  20       |  30       |  40       |  50       |  60       |  70       |  80
   1 AATTGTAATA CGACTCACTA TAGGGCGAAT TGGGTACCGG GCCCCCCCTC GAGGTCGACG GTATCGATAA GCTTGATATC 80
  81 GAATTCGGCA CGAGTTTTAC ACCATCACCA AAACCCAGAA TTTTATGATG AGATTAAAAT AGAGTTGCCC ACTCAGCTGC 160
 161 ATGAAAAGCA CCACCTGTTG CTCACATTCT TCCATGTCAG CTGTGACAAC TCAAGTAAAG GAAGCACGAA GAAGAGGGAT 240
 241 GTCGTTGAAA CCCAAGTTGG CTACTCCTGG CTTCCCCTCC TGAAAGACGG AAGGGTGGTG ACAAGCGAGC AGCACATCCC 320
 321 GGTCTCGGCG AACCTTCCTT CGGGCTATCT TGGCTACCAA GAGCTTGGGA TGGGCAGGCA TTATGGTCCG GAAATTAAAT 400
 401 GGGTAGATGG AGGCAAGCCA CTGCTGAAAA TTTCCACTCA TCTGGTTTCT ACAGGGATAC TCAGGATCAG CATTTACATA 480
 481 ATTTTTTCCA GTACTGTCAG AAAACCGAAT CTGGAGCCCA AGCCTTAGGA AACGAACTTG TAAAGTACCT TAAGAGTCTG 560
 561 CATGCGATGG AAGGCCACGT GATGATCGCC TTCTTGCCCA CTATCCTAAA CCAGCTGTTC CGAGTCCTCA CCAGAGCCAC 640
 641 ACAGGAAGAA GTCGCGGTTA ACGTGACTCG GGTCATTATT CATGTGGTTG CCCAGTGCCA TGAGGAAGGA TTGGAGAGCC 720
 721 ACTTGAGGTC ATATGTTAAG TACGCGTATA AGGCTGAGCC ATATGTTGCC TCTGAATACA AGACAGTGCA TGAAGAACTG 800
 801 ACCAAATCCA TGACCACGAT TCTCAAGCCT TCTGCCGATT TCCTCACCAG CAACAAACTA CTGAGGTACT CATGGTTTTT 880
 881 CTTTGATGTA CTGATCAAAT CTATGGCTCA GCATTTGATA GAGAACTCCA AAGTTAAGTT GCTGCGAAAC CAGAGATTTC 960
 961 CTGCATCCTA TCATCATGCA GCGGAAACCG TTGTAAATAT GCTGATGCCA CACATCACTC AGAAGTTTGG AGATAATCCA 1040
1041 GAGGCATCTA AGAACGCGAA TCATAGCCTT GCTGTCTTCA TCAAGAGATG TTTCACCTTC ATGGACAGGG GCTTTGTCTT 1120
1121 CAAGCAGATC AACAACTACA TTAGCTGTTT TGCTCCTGGA GACCCAAAGA CCCTCTTTGA ATACAAGTTT GAATTTCTCC 1200
1201 GTGTAGTGTG CAACCATGAA CATTATATTC CGTTGAACTT ACCAATGCCA TTTGGAAAAG GCAGGATTCA AAGATACCAA 1280
1281 GACCTCCAGC TTGACTACTC ATTAACAGAT GAGTTCTGCA GAAACCACTT CTTGGTGGGA CTGTTACTGA GGGAGGTGGG 1360
1361 GACAGCCCTC CAGGAGTTCC GGGAGGTCCG TCTGATCGCC ATCAGTGTGC TCAAGAACCT GCTGATAAAG CATTCTTTTG 1440
1441 ATGACAGATA TGCTTCAAGG AGCCATCAGG CAAGGATAGC CACCCTCTAC CTGCCTCTGT TTGGTCTGCT GATTGAAAAC 1520
1521 GTCCAGCGGA TCAATGTGAG GGATGTGTCA CCCTTCCCTG TGAACGCGGG CATGACCGTG AAGGATGAAT CCCTGGCTCT 1600
1601 ACCAGCTGTG AATCCGCTGG TGACGCCGCA GAAGGGAAGC ACCCTGGACA ACAGCCTGCA CAAGGACCTG CTGGGCGCCA 1680
1681 TCTCCGGCAT TGCTTCTCCA TATACAACCT CAACTCCAAA CATCAACAGT GTGAGAAATG CTGATTCGAG AGGATCTCTC 1760
1761 ATAAGCACAG ATTCGGGTAA CAGCCTTCCA GAAAGGAATA GTGAGAAGAG CAATTCCCTG GATAAGCACC AACAAAGTAG 1840
1841 CACATTGGGA AATTCCGTGG TTCGCTGTGA TAAACTTGAC CAGTCTGAGA TTAAGAGCCT ACTGATGTGT TTCCTCTACA 1920
1921 TCTTAAAGAG CATGTCTGAT GATGCTTTGT TTACATATTG GAACAAGGCT TCAACATCTG AACTTATGGA TTTTTTTACA 2000
2001 ATATCTGAAG TCTGCCTGCA CCAGTTCCAG TACATGGGGA AGCGATACAT AGCCAGGAAC CAGGAGGGGT TGGGACCCAT 2080
2081 AGTTCATGAT CGAAAGTCTC AGACATTGCC TGTTTCCCGT AACAGAACAG GAATGATGCA TGCCAGATTG CAGCAGCTGG 2160
2161 GCAGCCTGGA TAACTCTCTC ACTTTTAACC ACAGCTATGG CCACTCGGAC GCAGATGTTC TGCACCAGTC ATTACTTGAA 2240
2241 GCCAACATTG CTACTGAGGT TTGCCTGACA GCTCTGGACA CGCTTTCTCT ATTTACATTG GCGTTTAAGA ACCAGCTCCT 2320
2321 GGCCGACCAT GGACATAATC CTCTCATGAA AAAAGTTTTT GATGTCTACC TGTGTTTTCT TCAAAAACAT CAGTCTGAAA 2400
2401 CGGCTTTAAA AAATGTCTTC ACTGCCTTAA GGTCCTTAAT TTATAAGTTT CCCTCAACAT TCTATGAAGG GAGAGCGGAC 2480
2481 ATGTGTGCGG CTCTGTGTTA CGAGATTCTC AAGTGCTGTA ACTCCAAGCT GAGCTCCATC AGGACGGAGG CCTCCCAGCT 2560
2561 GCTCTACTTC CTGATGAGGA ACAACTTTGA TTACACTGGA AAGAAGTCCT TTGTCCGGAC ACATTTGCAA GTCATCATAT 2640
2641 CTGTCAGCCA GCTGATAGCA GACGTTGTTG GCATTGGGGA AACCAGATTC CAGCAGTCCC TGTCCATCAT CAACAACTGT 2720
2721 GCCAACAGTG ACCGGCTTAT TAAGCACACC AGCTTCTCCT CTGATGTGAA GGACTTAACC AAAAGGATAC GCACGGTGCT 2800
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2961 GCAGCAATGT GCTATGTCCA CGTAACAGCC CTAGTGGCAG AATATCTCAC ACGGAAAGGC GTGTTTAGAC AAGGATGCAC 3040
3041 CGCCTTCAGG GTCATTACCC CAAACATCGA CGAGGAGGCC TCCATGATGG AAGACGTGGG GATGCAGGAT GTCCATTTCA 3120
3121 ACGAGGATGT GCTGATGGAG CTCCTTGAGC AGTGCGCAGA TGGACTCTGG AAAGCCGAGC GCTACGAGCT CATCGCCGAC 3200
3201 ATCTACAAAC TTATCATCCC CATTTATGAG AAGCGGAGGG ATTTCTTTGA AGATGAAGAT GGAAAGGAGT ATATTTACAA 3280
3281 GGAACCCAAA CTCACACCGC TGTCGGAAAT TTCTCAGAGA CTCCTTAAAC TGTACTCGGA TAAATTTGGT TCTGAAAATG 3360
3361 TCAAAATGAT ACAGGATTCT GGCAAGGTCA ACCCTAAGGA TCTGGATTCT AAGTATGCAT ACATCCAGGT GACTCACGTC 3440
3441 ATCCCCTTCT TTGACGAAAA AGAGTTGCAA GAAAGGAAAA CAGAGTTTGA GAGATCCCAC AACATCCGCC GCTTCATGTT 3520
3521 TGAGATGCCA TTTACGCAGA CCGGGAAGAG GCAGGGCGGG GTGGAAGAGC AGTGCAAACG GCGCACCATC CTGACAGCCA 3600
3601 TACACTGCTT CCCTTATGTG AAGAAGCGCA TCCCTGTCAT GTACCAGCAC CACACTGACC TGAACCCCAT CGAGGTGGCC 3680
3681 ATTGACGAGA TGAGTAAGAA GGTGGCGGAG CTCCGGCAGC TGTGCTCCTC GGCCGAGGTG GACATGATCA AACTGCAGCT 3760
3761 CAAACTCCAG GGCAGCGTGA GTGTTCAGGT CAATGCTGGC CCACTAGCAT ATGCGCGAGC TTTCTTAGAT GATACAAACA 3840
3841 CAAAGCGATA TCCTGACAAT AAAGTGAAGC TGCTTAAGGA AGTTTTCAGG CAATTTGTGG AAGCTTGCGG TCAAGCCTTA 3920
3921 GCGGTAAACG AACGTCTGAT TAAAGAAGAC CAGCTCGAGT ATCAGGAAGA AATGAAAGCC AACTACAGGG AAATGGCGAA 4000
4001 GGAGCTTTCT GAAATCATGC ATGAGCAGAT CTGCCCCCTG GAGGAGAAGA CGAGCGTCTT ACCGAATTCC CTTCACATCT 4080
4081 TCAACGCCAT CAGTGGGACT CCAACAAGCA CAATGGTTCA CGGGATGACC AGCTCGTCTT CGGTCGTGTG ATTACATCTC 4160
4161 ATGGCCCGTG TGTGGGGACT TGCTTTGTCA TTTGCAAACT CAGGATGCTT TCCAAAGCCA ATCACTGGGG AGACCGAGCA 4240
4241 CAGGGAGGAC CAAGGGGAAG GGGAGAGAAA GGAAATAAAG AACAACGTTA TTTCTTAACA GACTTTCTAT AGGAGTTGTA 4320
4321 AGAAGGTGCA CATATTTTTT TAAATCTCAC TGGCAATATT CAAAGTTTTC ATTGTGTCTT AACAAAGGTG TGGTAGACAC 4400
4401 TCTTGAGCTG GACTTAGATT TTATTCTTCC TTGCAGAGTA GTGTTAGAAT AGATGGCCTA CAGAAAAAAA AGGTTCTGGG 4480
4481 ATCTACATGG CAGGGAGGGC TGCACTGACA TTGATGCCTG GGGGACCTTT TGCCTCGACT CGTGCCGGAA ATCTGATCGT 4560
4561 AATCAGGGTA CAGAACTTAC TAGTTTTGTC TAGGAGTATG TTGTATGACT AGGATTTGTG CTATTATCTC ATTCAACAAC 4640
4641 ATAGAGCAAG AATAGTGAGC TAACTGAGCT AGACACTCAA TTAATCCGCT ACTGGCTTCA AGTCAGAACT TTGTCATTAA 4720
4721 TCATCGACTC CGGGACGGTC ATATATGTAT TACATTTCTA CATTTTTAAT ACTCACATGG GCTTATGCAT TAAGTTTAAT 4800
4801 TGTGATAAAT TTGTGCTGGT CCAGTATATG CAATACACTT TAATGGTTTA TTCTTGTCAT AAAAATGTGC AATATGGAGA 4880
4881 TGTATACAAG TCTTTACT                                                                    4898
          |  10       |  20       |  30       |  40       |  50       |  60       |  70       |  80
```

FIG.10C

```
        |   10      |   20      |   30      |   40      |   50      |   60      |   70      |   80
   1 MEGHVMIAFL PTILNQLFRV LTRATQEEVA VNVTRVIIHV VAQCHEEGLE SHLRSYVKYA YKAEPYVASE YKTVHEELTK 80
  81 SMTTILKPSA DFLTSNKLLR YSWFFFDVLI KSMAQHLIEN SKVKLLRNQR FPASYHHAAE TVVNMLMPHI TQKFGDNPEA 160
 161 SKNANHSLAV FIKRCFTFMD RGEVFKQINN YISCFAPGDP KTLFEYKFEF LRVVCNHEHY IPLNLPMPFG KGRIQRYQDL 240
 241 QLDYSLTDEF CRNHFLVGLL LREVGTALQE FREVRLIAIS VLKNLLIKHS FDDRYASRSH QARIATLYLP LFGLLIENVQ 320
 321 RINVRDVSPF PVNAGMTVKD ESLALPAVNP LVTPQKGSTL DNSLHKDLLG AISGIASPYT TSTPNINSVR NADSRGSLIS 400
 401 TDSGNSLPER NSEKSNSLDK HQQSSTLGNS VVRCDKLDQS EIKSLLMCFL YILKSMSDDA LFTYWNKAST SELMDFFTIS 480
 481 EVCLHQFQYM GKRYIARNQE GLGPIVHDRK SQTLPVSRNR TGMMHARLQQ LGSLDNSLTF NHSYGHSDAD VLHQSLLEAN 560
 561 IATEVCLTAL DTLSLFTLAF KNQLLADHGH NPLMKKVFDV YLCFLQKHQS ETALKNVFTA LRSLIYKFPS TFYEGRADMC 640
 641 AALCYEILKC CNSKLSSIRT EASQLLYFLM RNNFDYTGKK SFVRTHLQVI ISVSQLIADV VGIGETRFQQ SLSIINNCAN 720
 721 SDRLIKHTSF SSDVKDLTKR IRTVLMATAQ MKEHENDPEM LVDLQYSLAK SYASTPELRK TWLDSMARIH VKNGDLSEAA 800
 801 MCYVHVTALV AEYLTRKGVF RQGCTAFRVI TPNIDEEASM MEDVGMQDVH FNEDVLMELL EQCADGLWKA ERYELIADIY 880
 881 KLIIPIYEKR RDFFEDEDGK EYIYKEPKLT PLSEISQRLL KLYSDKFGSE NVKMIQDSGK VNPKDLDSKY AYIQVTHVIP 960
 961 FFDEKELQER KTEFERSHNI RRFMFEMPFT QTGKRQGGVE EQCKRRTILT AIHCFPYVKK RIPVMYQHHT DLNPIEVAID 1040
1041 EMSKKVAELR QLCSSAEVDM IKLQLKLQGS VSVQVNAGPL AYARAFLDDT NTKRYPDNKV KLLKEVFRQF VEACGQALAV 1120
1121 NERLIKEDQL EYQEEMKANY REMAKELSEI MHEQICPLEE KTSVLPNSLH IFNAISGTPT STMVHGMTSS SSVV      1195
        |   10      |   20      |   30      |   40      |   50      |   60      |   70      |   80
```

FIG. 10C (cont.)

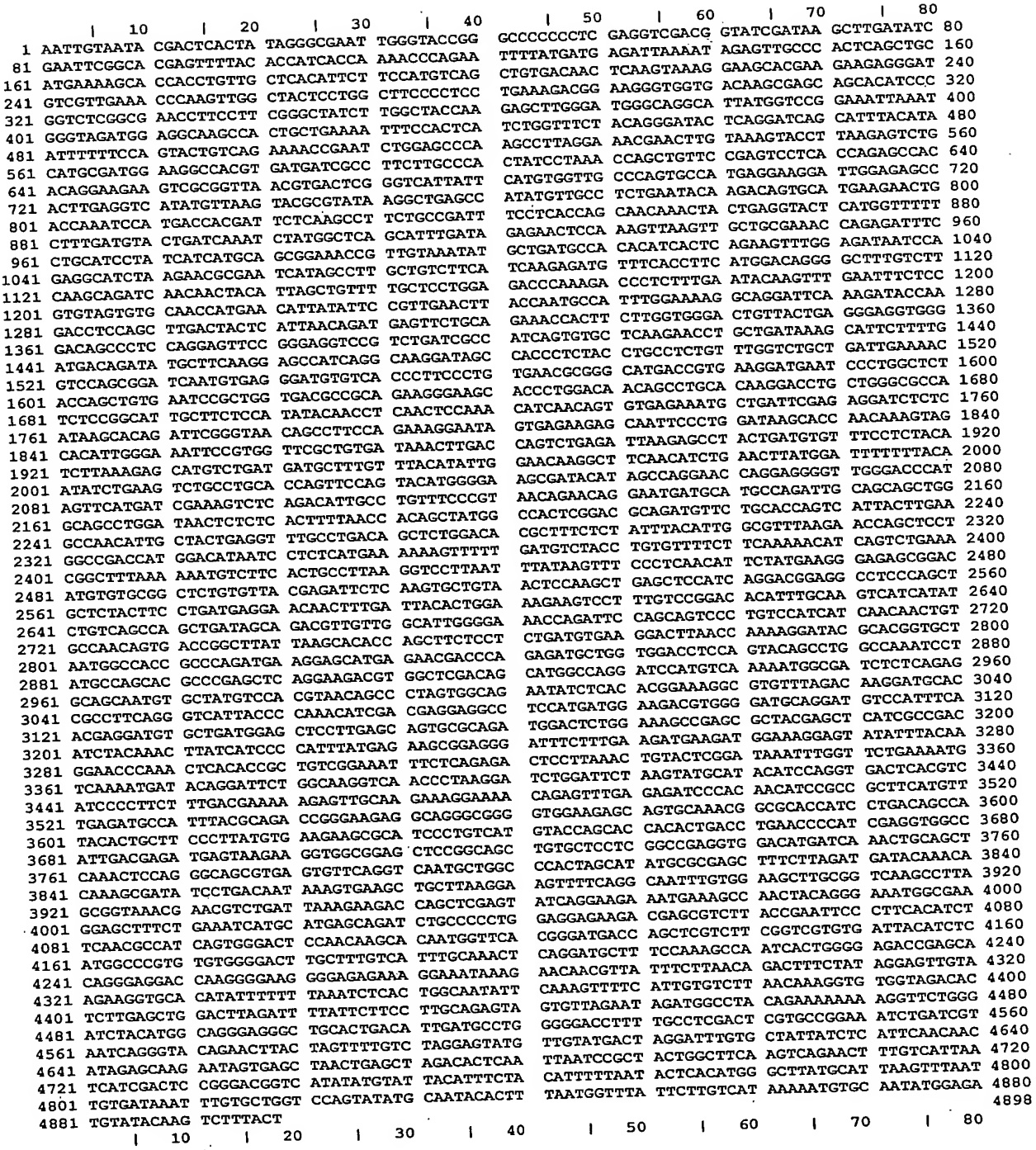

FIG.10D

```
          |   10      |   20      |   30      |   40      |   50      |   60      |   70      |   80
  1 MEGHVMIAFL PTILNQLFRV LTRATQEEVA VNVTRVIIHV VAQCHEEGLE SHLRSYVKYA YKAEPYVASE YKTVHEELTK 80
 81 SMTTILKPSA DFLTSNKLLR YSWFFFDVLI KSMAQHLIEN SKVKLLRNQR FPASYHHAAE TVVNMLMPHI TQKFGDNPEA 160
161 SKNANHSLAV FIKRCFTFMD RGFVFKQINN YISCFAPGDP KTLFEYKFEF LRVVCNHEHY IPLNLPMPFG KGRIQRYQDL 240
241 QLDYSLTDEF CRNHFLVGLL LREVGTALQE FREVRLIAIS VLKNLLIKHS FDDRYASRSH QARIATLYLP LFGLLIENVQ 320
321 RINVRDVSPF PVNAGMTVKD ESLALPAVNP LVTPQKGSTL DNSLHKDLLG AISGIASPYT TSTPNINSVR NADSRGSLIS 400
401 TDSGNSLPER NSEKSNSLDK HQQSSTLGNS VVRCDKLDQS EIKSLLMCFL YILKSMSDDA LFTYWNKAST SELMDFFTIS 480
481 EVCLHQFQYM GKRYIARNQE GLGPIVHDRK SQTLPVSRNR TGMMHARLQQ LGSLDNSLTF NHSYGHSDAD VLHQSLLEAN 560
561 IATEVCLTAL DTLSLFTLAF KNQLLADHGH NPLMKKVFDV YLCFLQKHQS ETALKNVFTA LRSLIYKFPS TFYEGRADMC 640
641 AALCYEILKC CNSKLSSIRT EASQLLYFLM RNNFDYTGKK SFVRTHLQVI ISVSQLIADV VGIGETRFQQ SLSIINNCAN 720
721 SDRLIKHTSF SSDVKDLTKR IRTVLMATAQ MKEHENDPEM LVDLQYSLAK SYASTPELRK TWLDSMARIH VKNGDLSEAA 800
801 MCYVHVTALV AEYLTRKGVF RQGCTAFRVI TPNIDEEASM MEDVGMQDVH FNEDVLMELL EQCADGLWKA ERYELIADIY 880
881 KLIIPIYEKR RDFFEDEDGK EYIYKEPKLT PLSEISQRLL KLYSDKFGSE NVKMIQDSGK VNPKDLDSKY AYIQVTHVIP 960
961 FFDEKELQER KTEFERSHNI RRFMFEMPFT QTGKRQGGVE EQCKRRTILT AIHCFPYVKK RIPVMYQHHT DLNPIEVAID 1040
1041 EMSKKVAELR QLCSSAEVDM IKLQLKLQGS VSVQVNAGPL AYARAFLDDT NTKRYPDNKV KLLKEVFRQF VEACGQALAV 1120
1121 NERLIKEDQL EYQEEMKANY REMAKELSEI MHEQICPLEE KTSVLPNSLH IFNAISGTPT STMVHGMTSS SSVV      1195
          |   10      |   20      |   30      |   40      |   50      |   60      |   70      |   80
```

FIG. 10D(cont.)

```
        |  10      |  20      |  30      |  40      |  50      |  60      |  70      |  80
  1 AATTGTAATA CGACTCACTA TAGGGCGAAT TGGGTACCGG  GCCCCCCCTC GAGGTCGACG GTATCGATAA GCTTGATATC  80
 81 GAATTCGGCA CGAGTTTTAC ACCATCACCA AAACCCAGAA  TTTTATGATG AGATTAAAAT AGAGTTGCCC ACTCAGCTGC 160
161 ATGAAAAGCA CCACCTGTTG CTCACATTCT TCCATGTCAG  CTGTGACAAC TCAAGTAAAG GAAGCACGAA GAAGAGGGAT 240
241 GTCGTTGAAA CCCAAGTTGG CTACTCCTGG CTTCCCCTCC  TGAAAGACGG AAGGGTGGTG ACAAGCGAGC AGCACATCCC 320
321 GGTCTCGGCG AACCTTCCTT CGGGCTATCT TGGCTACCAA  GAGCTTGGGA TGGGCAGGCA TTATGGTCCG GAAATTAAAT 400
401 GGGTAGATGG AGGCAAGCCA CTGCTGAAAA TTTCCACTCA  TCTGGTTTCT ACAGGGATAC TCAGGATCAG CATTTACATA 480
481 ATTTTTTCCA GTACTGTCAG AAAACCGAAT CTGGAGCCCA  AGCCTTAGGA AACGAACTTG TAAAGTACCT TAAGAGTCTG 560
561 CATGCGATGG AAGGCCACGT GATGATCGCC TTCTTGCCCA  CTATCCTAAA CCAGCTGTTC CGAGTCCTCA CCAGAGCCAC 640
641 ACAGGAAGAA GTCGCGGTTA ACGTGACTCG GGTCATTATT  CATGTGGTTG CCCAGTGCCA TGAGGAAGGA TTGGAGAGCC 720
721 ACTTGAGGTC ATATGTTAAG TACGCGTATA AGGCTGAGCC  ATATGTTGCC TCTGAATACA AGACAGTGCA TGAAGAACTG 800
801 ACCAAATCCA TGACCACGAT TCTCAAGCCT TCTGCCGATT  TCCTCACCAG CAACAAACTA CTGAGGTACT CATGGTTTTT 880
881 CTTTGATGTA CTGATCAAAT CTATGGCTCA GCATTTGATA  GAGAACTCCA AAGTTAAGTT GCTGCGAAAC CAGAGATTTC 960
961 CTGCATCCTA TCATCATGCA GCGGAAACCG TTGTAAATAT  GCTGATGCCA CACATCACTC AGAAGTTTGG AGATAATCCA 1040
1041 GAGGCATCTA AGAACGCGAA TCATAGCCTT GCTGTCTTCA  TCAAGAGATG TTTCACCTTC ATGGACAGGG GCTTTGTCTT 1120
1121 CAAGCAGATC AACAACTACA TTAGCTGTTT TGCTCCTGGA  GACCCAAAGA CCCTCTTTGA ATACAAGTTT GAATTTCTCC 1200
1201 GTGTAGTGTG CAACCATGAA CATTATATTC CGTTGAACTT  ACCAATGCCA TTTGGAAAAG GCAGGATTCA AAGATACCAA 1280
1281 GACCTCCAGC TTGACTACTC ATTAACAGAT GAGTTCTGCA  GAAACCACTT CTTGGTGGGA CTGTTACTGA GGGAGGTGGG 1360
1361 GACAGCCCTC CAGGAGTTCC GGGAGGTCCG TCTGATCGCC  ATCAGTGTGC TCAAGAACCT GCTGATAAAG CATTCTTTTG 1440
1441 ATGACAGATA TGCTTCAGGA AGCCATCAGG CAAGGATAGC  CACCCTCTAC CTGCCTCTGT TTGGTCTGCT GATTGAAAAC 1520
1521 GTCCAGCGGA TCAATGTGAG GGATGTGTCA CCCTTCCCTG  TGAACGCGGG CATGACCGTG AAGGATGAAT CCCTGGCTCT 1600
1601 ACCAGCTGTG AATCCGCTGG TGACGCCGCA GAAGGGAAGC  ACCCTGGACA ACAGCCTGCA CAAGGACCTG CTGGGCGCCA 1680
1681 TCTCCGGCAT TGCTTCTCCA TATACAACCT CAACTCCAAA  CATCAACAGT GTGAGAAATG CTGATTCGAG AGGATCTCTC 1760
1761 ATAAGCACAG ATTCGGGTAA CAGCCTTCCA GAAAGGAATA  GTGAGAAGAG CAATTCCCTG GATAAGCACC AACAAAGTAG 1840
1841 CACATTGGGA AATTCCGTGG TTCGCTGTGA TAAACTTGAC  CAGTCTGAGA TTAAGAGCCT ACTGATGTGT TTCCTCTACA 1920
1921 TCTTAAAGAG CATGTCTGAT GATGCTTTGT TTACATATTG  GAACAAGGCT TCAACATCTG AACTTATGGA TTTTTTTACA 2000
2001 ATATCTGAAG TCTGCCTGCA CCAGTTCCAG TACATGGGGA  AGCGATACAT AGCCAGGAAC CAGGAGGGGT TGGGACCCAT 2080
2081 AGTTCATGAT CGAAAGTCTC AGACATTGCC TGTTTCCCGT  AACAGAACAG GAATGATGCA TGCCAGATTG CAGCAGCTGG 2160
2161 GCAGCCTGGA TAACTCTCTC ACTTTTAACC ACAGCTATGG  CCACTCGGAC GCAGATGTTC TGCACCAGTC ATTACTTGAA 2240
2241 GCCAACATTG CTACTGAGGT TTGCCTGACA GCTCTGGACA  CGCTTTCTCT ATTTACATTG GCGTTTAAGA ACCAGCTCCT 2320
2321 GGCCGACCAT GGACATAATC CTCTCATGAA AAAAGTTTTT  GATGTCTACC TGTGTTTTCT TCAAAAACAT CAGTCTGAAA 2400
2401 CGGCTTTAAA AAATGTCTTC ACTGCCTTAA GGTCCTTAAT  TTATAAGTTT CCCTCAACAT TCTATGAAGG GAGAGCGGAC 2480
2481 ATGTGTGCGG CTCTGTGTTA CGAGATTCTC AAGTGCTGTA  ACTCCAAGCT GAGCTCCATC AGGACGGAGG CCTCCCAGCT 2560
2561 GCTCTACTTC CTGATGAGGA ACAACTTTGA TTACACTGGA  AAGAAGTCCT TTGTCCGGAC ACATTTGCAA GTCATCATAT 2640
2641 CTGTCAGCCA GCTGATAGCA GACGTTGTTG GCATTGGGGA  AACCAGATTC CAGCAGTCCC TGTCCATCAT CAACAACTGT 2720
2721 GCCAACAGTG ACCGGCTTAT TAAGCACACC AGCTTCTCCT  CTGATGTGAA GGACTTAACC AAAAGGATAC GCACGGTGCT 2800
2801 AATGGCCACC GCCCAGATGA AGGAGCATGA GAACGACCCA  GAGATGCTGG TGGACCTCCA GTACAGCCTG GCCAAATCCT 2880
2881 ATGCCAGCAC GCCCGAGCTC AGGAAGACGT GGCTCGACAG  CATGGCCAGG ATCCATGTCA AAAATGGCGA TCTCTCAGAG 2960
2961 GCAGCAATGT GCTATGTCCA CGTAACAGCC CTAGTGGCAG  AATATCTCAC ACGGAAAGGC GTGTTTAGAC AAGGATGCAC 3040
3041 CGCCTTCAGG GTCATTACCC CAAACATCGA CGAGGAGGCC  TCCATGATGG AAGACGTGGG GATGCAGGAT GTCCATTTCA 3120
3121 ACGAGGATGT GCTGATGGAG CTCCTTGAGC AGTGCGCAGA  TGGACTCTGG AAAGCCGAGC GCTACGAGCT CATCGCCGAC 3200
3201 ATCTACAAAC TTATCATCCC CATTTATGAG AAGCGGAGGG  ATTTCTTTGA AGATGAAGAT GGAAAGGAGT ATATTTACAA 3280
3281 GGAACCCAAA CTCACACCGC TGTCGGAAAT TTCTCAGAGA  CTCCTTAAAC TGTACTCGGA TAAATTTGGT TCTGAAAATG 3360
3361 TCAAAATGAT ACAGGATTCT GGCAAGGTCA ACCCTAAGGA  TCTGGATTCT AAGTATGCAT ACATCCAGGT GACTCACGTC 3440
3441 ATCCCCTTCT TTGACGAAAA AGAGTTGCAA GAAAGGAAAA  CAGAGTTTGA GAGATCCCAC AACATCCGCC GCTTCATGTT 3520
3521 TGAGATGCCA TTTACGCAGA CCGGGAAGAG GCAGGGCGGG  GTGGAAGAGC AGTGCAAACG GCGCACCATC CTGACAGCCA 3600
3601 TACACTGCTT CCCTTATGTG AAGAAGCGCA TCCCTGTCAT  GTACCAGCAC CACACTGACC TGAACCCCAT CGAGGTGGCC 3680
3681 ATTGACGAGA TGAGTAAGAA GGTGGCGGAG CTCCGGCAGC  TGTGCTCCTC GGCCGAGGTG GACATGATCA AACTGCAGCT 3760
3761 CAAACTCCAG GGCAGCGTGA GTGTTCAGGT CAATGCTGGC  CCACTAGCAT ATGCGCGAGC TTTCTTAGAT GATACAAACA 3840
3841 CAAAGCGATA TCCTGACAAT AAAGTGAAGC TGCTTAAGGA  AGTTTTCAGG CAATTTGTGG AAGCTTGCGG TCAAGCCTTA 3920
3921 GCGGTAAACG AACGTCTGAT TAAAGAAGAC CAGCTCGAGT  ATCAGGAAGA AATGAAAGCC AACTACAGGG AAATGGCGAA 4000
4001 GGAGCTTTCT GAAATCATGC ATGAGCAGAT CTGCCCCCTG  GAGGAGAAGA CGAGCGTCTT ACCGAATTCC CTTCACATCT 4080
4081 TCAACGCCAT CAGTGGGACT CCAACAAGCA CAATGGTTCA  CGGGATGACC AGCTCGTCTT CGGTCGTGTG ATTACATCTC 4160
4161 ATGGCCCGTG TGTGGGGACT TGCTTTGTCA TTTGCAAACT  CAGGATGCTT TCCAAAGCCA ATCACTGGGG AGACCGAGCA 4240
4241 CAGGGAGGAC CAAGGGGAAG GGGAGAGAAA GGAAATAAAG  AACAACGTTA TTTCTTAACA GACTTTCTAT AGGAGTTGTA 4320
4321 AGAAGGTGCA CATATTTTTT TAAATCTCAC TGGCAATATT  CAAAGTTTTC ATTGTGTCTT AACAAAGGTG TGGTAGACAC 4400
4401 TCTTGAGCTG GACTTAGATT TTATTCTTCC TTGCAGAGTA  GTGTTAGAAT AGATGGCCTA CAGAAAAAAA AGGTTCTGGG 4480
4481 ATCTACATGG CAGGGAGGGC TGCACTGACA TTGATGCCTG  GGGGACCTTT TGCCTCGACT CGTGCCGGAA ATCTGATCGT 4560
4561 AATCAGGGTA CAGAACTTAC TAGTTTTGTC TAGGAGTATG  TTGTATGACT AGGATTTGTG CTATTATCTC ATTCAACAAC 4640
4641 ATAGAGCAAG AATAGTGAGC TAACTGAGCT AGACACTCAA  TTAATCCGCT ACTGGCTTCA AGTCAGAACT TTGTCATTAA 4720
4721 TCATCGACTC CGGGACGGTC ATATATGTAT TACATTTCTA  CATTTTTAAT ACTCACATGG GCTTATGCAT TAAGTTTAAT 4800
4801 TGTGATAAAT TTGTGCTGGT CCAGTATATG CAATACACTT  TAATGGTTTA TTCTTGTCAT AAAAATGTGC AATATGGAGA 4880
4881 TGTATACAAG TCTTTACT                                                                    4898
        |  10      |  20      |  30      |  40      |  50      |  60      |  70      |  80
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FIG.10E

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          |  10       |  20       |  30       |  40       |  50       |  60       |  70       |  80
  1 MEGHVMIAFL PTILNQLFRV LTRATQEEVA VNVTRVIIHV  VAQCHEEGLE SHLRSYVKYA YKAEPYVASE YKTVHEELTK 80
 81 SMTTILKPSA DFLTSNKLLR YSWFFFDVLI KSMAQHLIEN  SKVKLLRNQR FPASYHHAAE TVVNMLMPHI TQKFGDNPEA 160
161 SKNANHSLAV FIKRCFTFMD RGFVFKQINN YISCFAPGDP  KTLFEYKFEF LRVVCNHEHY IPLNLPMPFG KGRIQRYQDL 240
241 QLDYSLTDEF CRNHFLVGLL LREVGTALQE FREVRLIAIS  VLKNLLIKHS FDDRYASRSH QARIATLYLP LFGLLIENVQ 320
321 RINVRDVSPF PVNAGMTVKD ESLALPAVNP LVTPQKGSTL  DNSLHKDLLG AISGIASPYT TSTPNINSVR NADSRGSLIS 400
401 TDSGNSLPER NSEKSNSLDK HQQSSTLGNS VVRCDKLDQS  EIKSLLMCFL YILKSMSDDA LFTYWNKAST SELMDFFTIS 480
481 EVCLHQFQYM GKRYIARNQE GLGPIVHDRK SQTLPVSRNR  TGMMHARLQQ LGSLDNSLTF NHSYGHSDAD VLHQSLLEAN 560
561 IATEVCLTAL DTLSLFTLAF KNQLLADHGH NPLMKKVFDV  YLCFLQKHQS ETALKNVFTA LRSLIYKFPS TFYEGRADMC 640
641 AALCYEILKC CNSKLSSIRT EASQLLYFLM RNNFDYTGKK  SFVRTHLQVI ISVSQLIADV VGIGETRFQQ SLSIINNCAN 720
721 SDRLIKHTSF SSDVKDLTKR IRTVLMATAQ MKEHENDPEM  LVDLQYSLAK SYASTPELRK TWLDSMARIH VKNGDLSEAA 800
801 MCYVHVTALV AEYLTRKGVF RQGCTAFRVI TPNIDEEASM  MEDVGMQDVH FNEDVLMELL EQCADGLWKA ERYELIADIY 880
881 KLIIPIYEKR RDFFEDEDGK EYIYKEPKLT PLSEISQRLL  KLYSDKFGSE NVKMIQDSGK VNPKDLDSKY AYIQVTHVIP 960
961 FFDEKELQER KTEFERSHNI RRFMFEMPFT QTGKRQGGVE  EQCKRRTILT AIHCFPYVKK RIPVMYQHHT DLNPIEVAID 1040
1041 EMSKKVAELR QLCSSAEVDM IKLQLKLQGS VSVQVNAGPL  AYARAFLDDT NTKRYPDNKV KLLKEVFRQF VEACGQALAV 1120
1121 NERLIKEDQL EYQEEMKANY REMAKELSEI MHEQICPLEE  KTSVLPNSLH IFNAISGTPT STMVHGMTSS SSVV       1195
          |  10       |  20       |  30       |  40       |  50       |  60       |  70       |  80
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FIG. 10E (cont.)

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        |  10      |  20      |  30      |  40      |  50      |  60      |  70      |  80
  1 AATTGTAATA CGACTCACTA TAGGGCGAAT TGGGTACCGG GCCCCCCCTC GAGGTCGACG GTATCGATAA GCTTGATATC 80
 81 GAATTCGGCA CGAGTTTTAC ACCATCACCA AAACCCAGAA TTTTATGATG AGATTAAAAT AGAGTTGCCC ACTCAGCTGC 160
161 ATGAAAAGCA CCACCTGTTG CTCACATTCT TCCATGTCAG CTGTGACAAC TCAAGTAAAG GAAGCACGAA GAAGAGGGAT 240
241 GTCGTTGAAA CCCAAGTTGG CTACTCCTGG CTTCCCCTCC TGAAAGACGG AAGGGTGGTG ACAAGCGAGC AGCACATCCC 320
321 GGTCTCGGCG AACCTTCCTT CGGGCTATCT TGGCTACCAA GAGCTTGGGA TGGGCAGGCA TTATGGTCCG GAAATTAAAT 400
401 GGGTAGATGG AGGCAAGCCA CTGCTGAAAA TTTCCACTCA TCTGGTTTCT ACAGGGATAC TCAGGATCAG CATTTACATA 480
481 ATTTTTTCCA GTACTGTCAG AAAACCGAAT CTGGAGCCCA AGCCTTAGGA AACGAACTTG TAAAGTACCT TAAGAGTCTG 560
561 CATGCGATGG AAGGCCACGT GATGATCGCC TTCTTGCCCA CTATCCTAAA CCAGCTGTTC CGAGTCCTCA CCAGAGCCAC 640
641 ACAGGAAGAA GTCGCGGTTA ACGTGACTCG GGTCATTATT CATGTGGTTG CCCAGTGCCA TGAGGAAGGA TTGGAGAGCC 720
721 ACTTGAGGTC ATATGTTAAG TACGCGTATA AGGCTGAGCC ATATGTTGCC TCTGAATACA AGACAGTGCA TGAAGAACTG 800
801 ACCAAATCCA TGACCACGAT TCTCAAGCCT TCTGCCGATT TCCTCACCAG CAACAAACTA CTGAGGTACT CATGGTTTTT 880
881 CTTTGATGTA CTGATCAAAT CTATGGCTCA GCATTTGATA GAGAACTCCA AAGTTAAGTT GCTGCGAAAC CAGAGATTTC 960
961 CTGCATCCTA TCATCATGCA GCGGAAACCG TTGTAAATAT GCTGATGCCA CACATCACTC AGAAGTTTGG AGATAATCCA 1040
1041 GAGGCATCTA AGAACGCGAA TCATAGCCTT GCTGTCTTCA TCAAGAGATG TTTCACCTTC ATGGACAGGG GCTTTGTCTT 1120
1121 CAAGCAGATC AACAACTACA TTAGCTGTTT TGCTCCTGGA GACCCAAAGA CCCTCTTTGA ATACAAGTTT GAATTTCTCC 1200
1201 GTGTAGTGTG CAACCATGAA CATTATATTC CGTTGAACTT ACCAATGCCA TTTGGAAAAG GCAGGATTCA AAGATACCAA 1280
1281 GACCTCCAGC TTGACTACTC ATTAACAGAT GAGTTCTGCA GAAACCACTT CTTGGTGGGA CTGTTACTGA GGGAGGTGGG 1360
1361 GACAGCCCTC CAGGAGTTCC GGGAGGTCCG TCTGATCGCC ATCAGTGTGC TCAAGAACCT GCTGATAAAG CATTCTTTTG 1440
1441 ATGACAGATA TGCTTCAAGG AGCCATCAGG CAAGGATAGC CACCCTCTAC CTGCCTCTGT TTGGTCTGCT GATTGAAAAC 1520
1521 GTCCAGCGGA TCAATGTGAG GGATGTGTCA CCCTTCCCTG TGAACGCGGG CATGACCGTG AAGGATGAAT CCCTGGCTCT 1600
1601 ACCAGCTGTG AATCCGCTGG TGACGCCGCA GAAGGGAAGC ACCCTGGACA ACAGCCTGCA CAAGGACCTG CTGGGCGCCA 1680
1681 TCTCCGGCAT TGCTTCTCCA TATACAACCT CAACTCCAAA CATCAACAGT GTGAGAAATG CTGATTCGAG AGGATCTCTC 1760
1761 ATAAGCACAG ATTCGGGTAA CAGCCTTCCA GAAAGGAATA GTGAGAAGAG CAATTCCCTG GATAAGCACC AACAAAGTAG 1840
1841 CACATTGGGA AATTCCGTGG TTCGCTGTGA TAAACTTGAC CAGTCTGAGA TTAAGAGCCT ACTGATGTGT TTCCTCTACA 1920
1921 TCTTAAAGAG CATGTCTGAT GATGCTTTGT TTACATATTG GAACAAGGCT TCAACATCTG AACTTATGGA TTTTTTTACA 2000
2001 ATATCTGAAG TCTGCCTGCA CCAGTTCCAG TACATGGGGA AGCGATACAT AGCCAGGAAC CAGGAGGGGT TGGGACCCAT 2080
2081 AGTTCATGAT CGAAAGTCTC AGACATTGCC TGTTTCCCGT AACAGAACAG GAATGATGCA TGCCAGATTG CAGCAGCTGG 2160
2161 GCAGCCTGGA TAACTCTCTC ACTTTTAACC ACAGCTATGG CCACTCGGAC GCAGATGTTC TGCACCAGTC ATTACTTGAA 2240
2241 GCCAACATTG CTACTGAGGT TTGCCTGACA GCTCTGGACA CGCTTTCTCT ATTTACATTG GCGTTTAAGA ACCAGCTCCT 2320
2321 GGCCGACCAT GGACATAATC CTCTCATGAA AAAAGTTTTT GATGTCTACC TGTGTTTTCT TCAAAAACAT CAGTCTGAAA 2400
2401 CGGCTTTAAA AAATGTCTTC ACTGCCTTAA GGTCCTTAAT TTATAAGTTT CCCTCAACAT TCTATGAAGG GAGAGCGGAC 2480
2481 ATGTGTGCGG CTCTGTGTTA CGAGATTCTC AAGTGCTGTA ACTCCAAGCT GAGCTCCATC AGGACGGAGG CCTCCCAGCT 2560
2561 GCTCTACTTC CTGATGAGGA ACAACTTTGA TTACACTGGA AAGAAGTCCT TTGTCCGGAC ACATTTGCAA GTCATCATAT 2640
2641 CTGTCAGCCA GCTGATAGCA GACGTTGTTG GCATTGGGGA AACCAGATTC CAGCAGTCCC TGTCCATCAT CAACAACTGT 2720
2721 GCCAACAGTG ACCGGCTTAT TAAGCACACC AGCTTCTCCT CTGATGTGAA GGACTTAACC AAAAGGATAC GCACGGTGCT 2800
2801 AATGGCCACC GCCCAGATGA AGGAGCATGA GAACGACCCA GAGATGCTGG TGGACCTCCA GTACAGCCTG GCCAAATCCT 2880
2881 ATGCCAGCAC GCCCGAGCTC AGGAAGACGT GGCTCGACAG CATGGCCAGG ATCCATGTCA AAAATGGCGA TCTCTCAGAG 2960
2961 GCAGCAATGT GCTATGTCCA CGTAACAGCC CTAGTGGCAG AATATCTCAC ACGGAAAGGC GTGTTTAGAC AAGGATGCAC 3040
3041 CGCCTTCAGG GTCATTACCC CAAACATCGA CGAGGAGGCC TCCATGATGC AAGACGTGGG GATGCAGGAT GTCCATTTCA 3120
3121 ACGAGGATGT GCTGATGGAG CTCCTTGAGC AGTGCGCAGA TGGACTCTGG AAAGCCGAGC GCTACGAGCT CATCGCCGAC 3200
3201 ATCTACAAAC TTATCATCCC CATTTATGAG AAGCGGAGGG ATTTCTTTGA AGATGAAGAT GGAAAGGAGT ATATTTACAA 3280
3281 GGAACCCAAA CTCACACCGC TGTCGGAAAT TTCTCAGAGA CTCCTTAAAC TGTACTCGGA TAAATTTGGT TCTGAAAATG 3360
3361 TCAAAATGAT ACAGGATTCT GGCAAGGTCA ACCCTAAGGA TCTGGATTCT AAGTATGCAT ACATCCAGGT GACTCACGTC 3440
3441 ATCCCCTTCT TTGACGAAAA AGAGTTGCAA GAAAGGAAAA CAGAGTTTGA GAGATCCCAC AACATCCGCC GCTTCATGTT 3520
3521 TGAGATGCCA TTTACGCAGA CCGGGAAGAG GCAGGGCGGG GTGGAAGAGC AGTGCAAACG GCGCACCATC CTGACAGCCA 3600
3601 TACACTGCTT CCCTTATGTG AAGAAGCGCA TCCCTGTCAT GTACCAGCAC CACACTGACC TGAACCCCAT CGAGGTGGCC 3680
3681 ATTGACGAGA TGAGTAAGAA GGTGGCGGAG CTCCGGCAGC TGTGCTCCTC GGCCGAGGTG GACATGATCA AACTGCAGCT 3760
3761 CAAACTCCAG GGCAGCGTGA GTGTTCAGGT CAATGCTGGC CCACTAGCAT ATGCGCGAGC TTTCTTAGAT GATACAAACA 3840
3841 CAAAGCGATA TCCTGACAAT AAAGTGAAGC TGCTTAAGGA AGTTTTCAGG CAATTTGTGG AAGCTTGCGG TCAAGCCTTA 3920
3921 GCGGTAAACG AACGTCTGAT TAAAGAAGAC CAGCTCGAGT ATCAGGAAGA AATGAAAGCC AACTACAGGG AAATGGCGAA 4000
4001 GGAGCTTTCT GAAATCATGC ATGAGCAGAT CTGCCCCCTG GAGGAGAAGA CGAGCGTCTT ACCGAATTCC CTTCACATCT 4080
4081 TCAACGCCAT CAGTGGGACT CCAACAAGCA CAATGGTTCA CGGGATGACC AGCTCGTCTT CGGTCGTGTG ATTACATCTC 4160
4161 ATGGCCCGTG TGTGGGGACT TGCTTTGTCA TTTGCAAACT CAGGATGCTT TCCAAAGCCA ATCACTGGGG AGACCGAGCA 4240
4241 CAGGGAGGAC CAAGGGGAAG GGGAGAGAAA GGAAATAAAG AACAACGTTA TTTCTTAACA GACTTTCTAT AGGAGTTGTA 4320
4321 AGAAGGTGCA CATATTTTTT TAAATCTCAC TGGCAATATT CAAAGTTTTC ATTGTGTCTT AACAAAGGTG TGGTAGACAC 4400
4401 TCTTGAGCTG GACTTAGATT TTATTCTTCC TTGCAGAGTA GTGTTAGAAT AGATGGCCTA CAGAAAAAAA AGGTTCTGGG 4480
4481 ATCTACATGG CAGGGAGGGC TGCACTGACA TTGATGCCTG GGGGACCTTT TGCCTCGACT CGTGCCGGAA ATCTGATCGT 4560
4561 AATCAGGGTA CAGAACTTAC TAGTTTTGTC TAGGAGTATG TTGTATGACT AGGATTTGTG CTATTATCTC ATTCAACAAC 4640
4641 ATAGAGCAAG AATAGTGAGC TAACTGAGCT AGACACTCAA TTAATCCGCT ACTGGCTTCA AGTCAGAACT TTGTCATTAA 4720
4721 TCATCGACTC CGGGACGGTC ATATATGTAT TACATTTCTA CATTTTTAAT ACTCACATGG GCTTATGCAT TAAGTTTAAT 4800
4801 TGTGATAAAT TTGTGCTGGT CCAGTATATG CAATACACTT TAATGGTTTA TTCTTGTCAT AAAAATGTGC AATATGGAGA 4880
4881 TGTATACAAG TCTTTACT                                                                  4898
        |  10      |  20      |  30      |  40      |  50      |  60      |  70      |  80
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FIG.10F

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        |   10      |   20      |   30      |   40      |   50      |   60      |   70      |   80
   1 MEGHVMIAFL PTILNQLFRV LTRATQEEVA VNVTRVIIHV VAQCHEEGLE SHLRSYVKYA YKAEPYVASE YKTVHEELTK 80
  81 SMTTILKPSA DFLTSNKLLR YSWFFFDVLI KSMAQHLIEN SKVKLLRNQR FPASYHHAAE TVVNMLMPHI TQKFGDNPEA 160
 161 SKNANHSLAV FIKRCFTFMD RGFVFKQINN YISCFAPGDP KTLFEYKFEF LRVVCNHEHY IPLNLPMPFG KGRIQRYQDL 240
 241 QLDYSLTDEF CRNHFLVGLL LREVGTAIQE FREVRLIAIS VLKNLLIKHS FDDRYASRSH QARIATLYLP LFGLLIENVQ 320
 321 RINVRDVSPF PVNAGMTVKD ESLALPAVNP LVTPQKGSTL DNSLHKDLLG AISGIASPYT TSTPNINSVR NADSRGSLIS 400
 401 TDSGNSLPER NSEKSNSLDK HQQSSTLGNS VVRCDKLDQS EIKSLLMCFL YILKSMSDDA LFTYWNKAST SELMDFFTIS 480
 481 EVCLHQFQYM GKRYIARNQE GLGPIVHDRK SQTLPVSRNR TGMMHARLQQ LGSLDNSLTF NHSYGHSDAD VLHQSLLEAN 560
 561 IATEVCLTAL DTLSLFTLAF KNQLLADHGH NPLMKKVFDV YLCFLQKHQS ETALKNVFTA LRSLIYKFPS TFYEGRADMC 640
 641 AALCYEILKC CNSKLSSIRT EASQLLYFLM RNNFDYTGKK SFVRTHLQVI ISVSQLIADV VGIGETRFQQ SLSIINNCAN 720
 721 SDRLIKHTSF SSDVKDLTKR IRTVLMATAQ MKEHENDPEM LVDLQYSLAK SYASTPELRK TWLDSMARIH VKNGDLSEAA 800
 801 MCYVHVTALV AEYLTRKGVF RQGCTAFRVI TPNIDEEASM MEDVGMQDVH FNEDVLMELL EQCADGLWKA ERYELIADIY 880
 881 KLIIPIYEKR RDFFEDEDGK EYIYKEPKLT PLSEISQRLL KLYSDKFGSE NVKMIQDSGK VNPKDLDSKY AYIQVTHVIP 960
 961 FFDEKELQER KTEFERSHNI RRFMFEMPFT QTGKRQGGVE EQCKRRTILT AIHCFPYVKK RIPVMYQHHT DLNPIEVAID 1040
1041 EMSKKVAELR QLCSSAEVDM IKLQLKLQGS VSVQVNAGPL AYARAFLDDT NTKRYPDNKV KLLKEVFRQF VEACGQALAV 1120
1121 NERLIKEDQL EYQEEMKANY REMAKELSEI MHEQICPLEE KTSVLPNSLH IFNAISGTPT STMVHGMTSS SSVV       1195
        |   10      |   20      |   30      |   40      |   50      |   60      |   70      |   80
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FIG. 10F (cont.)

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        |  10      |  20      |  30      |  40      |  50      |  60      |  70      |  80
  1 AATTGTAATA CGACTCACTA TAGGGCGAAT TGGGTACCGG GCCCCCCCTC GAGGTCGACG GTATCGATAA GCTTGATATC 80
 81 GAATTCGGCA CGAGTTTTAC ACCATCACCA AAACCCAGAA TTTTATGATG AGATTAAAAT AGAGTTGCCC ACTCAGCTGC 160
161 ATGAAAAGCA CCACCTGTTG CTCACATTCT TCCATGTCAG CTGTGACAAC TCAAGTAAAG GAAGCACGAA GAAGAGGGAT 240
241 GTCGTTGAAA CCCAAGTTGG CTACTCCTGG CTTCCCCTCC TGAAAGACGG AAGGGTGGTG ACAAGCGAGC AGCACATCCC 320
321 GGTCTCGGCG AACCTTCCTT CGGGCTATCT TGGCTACCAA GAGCTTGGGA TGGGCAGGCA TTATGGTCCG GAAATTAAAT 400
401 GGGTAGATGG AGGCAAGCCA CTGCTGAAAA TTTCCACTCA TCTGGTTTCT ACAGGGATAC TCAGGATCAG CATTTACATA 480
481 ATTTTTTCCA GTACTGTCAG AAAACCGAAT CTGGAGCCCA AGCCTTAGGA AACGAACTTG TAAAGTACCT TAAGAGTCTG 560
561 CATGCGATGG AAGGCCACGT GATGATCGCC TTCTTGCCCA CTATCCTAAA CCAGCTGTTC CGAGTCCTCA CCAGAGCCAC 640
641 ACAGGAAGAA GTCGCGGTTA ACGTGACTCG GGTCATTATT CATGTGGTTG CCCAGTGCCA TGAGGAAGGA TTGGAGAGCC 720
721 ACTTGAGGTC ATATGTTAAG TACGCGTATA AGGCTGAGCC ATATGTTGCC TCTGAATACA AGACAGTGCA TGAAGAACTG 800
801 ACCAAATCCA TGACCACGAT TCTCAAGCCT TCTGCCGATT TCCTCACCAG CAACAAACTA CTGAGGTACT CATGGTTTTT 880
881 CTTTGATGTA CTGATCAAAT CTATGGCTCA GCATTTGATA GAGAACTCCA AAGTTAAGTT GCTGCGAAAC CAGAGATTTC 960
961 CTGCATCCTA TCATCATGCA GCGGAAACCG TTGTAAATAT GCTGATGCCA CACATCACTC AGAAGTTTGG AGATAATCCA 1040
1041 GAGGCATCTA AGAACGCGAA TCATAGCCTT GCTGTCTTCA TCAAGAGATG TTTCACCTTC ATGGACAGGG GCTTTGTCTT 1120
1121 CAAGCAGATC AACAACTACA TTAGCTGTTT TGCTCCTGGA GACCCAAAGA CCCTCTTTGA ATACAAGTTT GAATTTCTCC 1200
1201 GTGTAGTGTG CAACCATGAA CATTATATTC CGTTGAACTT ACCAATGCCA TTTGGAAAAG GCAGGATTCA AAGATACCAA 1280
1281 GACCTCCAGC TTGACTACTC ATTAACAGAT GAGTTCTGCA GAAACCACTT CTTGGTGGGA CTGTTACTGA GGGAGGTGGG 1360
1361 GACAGCCCTC CAGGAGTTCC GGGAGGTCCG TCTGATCGCC ATCAGTGTGC TCAAGAACCT GCTGATAAAG CATTCTTTTG 1440
1441 ATGACAGATA TGCTTCAAGG AGCCATCAGG CAAGGATAGC CACCCTCTAC CTGCCTCTGT TTGGTCTGCT GATTGAAAAC 1520
1521 GTCCAGCGGA TCAATGTGAG GGATGTGTCA CCCTTCCCTG TGAACGCGGG CATGACCGTG AAGGATGAAT CCCTGGCTCT 1600
1601 ACCAGCTGTG AATCCGCTGG TGACGCCGCA GAAGGGAAGC ACCCTGGACA ACAGCCTGCA CAAGGACCTG CTGGGCGCCA 1680
1681 TCTCCGGCAT TGCTTCTCCA TATACAACCT CAACTCCAAA CATCAACAGT GTGAGAAATG CTGATTCGAG AGGATCTCTC 1760
1761 ATAAGCACAG ATTCGGGTAA CAGCCTTCCA GAAAGGAATA GTGAGAAGAG CAATTCCCTG GATAAGCACC AACAAAGTAG 1840
1841 CACATTGGGA AATTCCGTGG TTCGCTGTGA TAAACTTGAC CAGTCTGAGA TTAAGAGCCT ACTGATGTGT TTCCTCTACA 1920
1921 TCTTAAAGAG CATGTCTGAT GATGCTTTGT TTACATATTG GAACAAGGCT TCAACATCTG AACTTATGGA TTTTTTTACA 2000
2001 ATATCTGAAG TCTGCCTGCA CCAGTTCCAG TACATGGGGA AGCGATACAT AGCCAGGAAC CAGGAGGGGT TGGGACCCAT 2080
2081 AGTTCATGAT CGAAAGTCTC AGACATTGCC TGTTTCCCGT AACAGAACAG GAATGATGCA TGCCAGATTG CAGCAGCTGG 2160
2161 GCAGCCTGGA TAACTCTCTC ACTTTTAACC ACAGCTATGG CCACTCGGAC GCAGATGTTC TGCACCAGTC ATTACTTGAA 2240
2241 GCCAACATTG CTACTGAGGT TTGCCTGACA GCTCTGGACA CGCTTTCTCT ATTTACATTG GCGTTTAAGA ACCAGCTCCT 2320
2321 GGCCGACCAT GGACATAATC CTCTCATGAA AAAAGTTTTT GATGTCTACC TGTGTTTTCT TCAAAAACAT CAGTCTGAAA 2400
2401 CGGCTTTAAA AAATGTCTTC ACTGCCTTAA GGTCCTTAAT TTATAAGTTT CCCTCAACAT TCTATGAAGG GAGAGCGGAC 2480
2481 ATGTGTGCGG CTCTGTGTTA CGAGATTCTC AAGTGCTGTA ACTCCAAGCT GAGCTCCATC AGGACGGAGG CCTCCCAGCT 2560
2561 GCTCTACTTC CTGATGAGGA ACAACTTTGA TTACACTGGA AAGAAGTCCT TTGTCCGGAC ACATTTGCAA GTCATCATAT 2640
2641 CTGTCAGCCA GCTGATAGCA GACGTTGTTG GCATTGGGGA AACCAGATTC CAGCAGTCCC TGTCCATCAT CAACAACTGT 2720
2721 GCCAACAGTG ACCGGCTTAT TAAGCACACC AGCTTCTCCT CTGATGTGAA GGACTTAACC AAAAGGATAC GCACGGTGCT 2800
2801 AATGGCCACC GCCCAGATGA AGGAGCATGA GAACGACCCA GAGATGCTGG TGGACCTCCA GTACAGCCTG GCCAAATCCT 2880
2881 ATGCCAGCAC GCCCGAGCTC AGGAAGACGT GGCTCGACAG CATGGCCAGG ATCCATGTCA AAAATGGCGA TCTCTCAGAG 2960
2961 GCAGCAATGT GCTATGTCCA CGTAACAGCC CTAGTGGCAG AATATCTCAC ACGGAAAGGC GTGTTTAGAC AAGGATGCAC 3040
3041 CGCCTTCAGG GTCATTACCC CAAACATCGA CGAGGAGGCC TCCATGATGG AAGACGTGGG GATGCAGGAT GTCCATTTCA 3120
3121 ACGAGGATGT GCTGATGGAG CTCCTTGAGC AGTGCGCAGA TGGACTCTGG AAAGCCGAGC GCTACGAGCT CATCGCCGAC 3200
3201 ATCTACAAAC TTATCATCCC CATTTATGAG AAGCGGAGGG ATTTCTTTGA AGATGAAGAT GGAAAGGAGT ATATTTACAA 3280
3281 GGAACCCAAA CTCACACCGC TGTCGGAAAT TTCTCAGAGA CTCCTTAAAC TGTACTCGGA TAAATTTGGT TCTGAAAATG 3360
3361 TCAAAATGAT ACAGGATTCT GGCAAGGTCA ACCCTAAGGA TCTGGATTCT AAGTATGCAT ACATCCAGGT GACTCACGTC 3440
3441 ATCCCCTTCT TTGACGAAAA AGAGTTGCAA GAAAGGAAAA CAGAGTTTGA GAGATCCCAC AACATCCGCC GCTTCATGTT 3520
3521 TGAGATGCCA TTTACGCAGA CCGGGAAGAG GCAGGGCGGG GTGGAAGAGC AGTGCAAACG GCGCACCATC CTGACAGCCA 3600
3601 TACACTGCTT CCCTTATGTG AAGAAGCGCA TCCCTGTCAT GTACCAGCAC CACACTGACC TGAACCCCAT CGAGGTGGCC 3680
3681 ATTGACGAGA TGAGTAAGAA GGTGGCGGAG CTCCGGCAGC TGTGCTCCTC GGCCGAGGTG GACATGATCA AACTGCAGCT 3760
3761 CAAACTCCAG GGCAGCGTGA GTGTTCAGGT CAATGCTGGC CCACTAGCAT ATGCGCGAGC TTTCTTAGAT GATACAAACA 3840
3841 CAAAGCGATA TCCTGACAAT AAAGTGAAGC TGCTTAAGGA AGTTTTCAGG CAATTTGTGG AAGCTTGCGG TCAAGCCTTA 3920
3921 GCGGTAAACG AACGTCTGAT TAAAGAAGAC CAGCTCGAGT ATCAGGAAGA AATGAAAGCC AACTACAGGG AAATGGCGAA 4000
4001 GGAGCTTTCT GAAATCATGC ATGAGCAGAT CTGCCCCCTG GAGGAGAAGA CGAGCGTCTT ACCGAATTCC CTTCACATCT 4080
4081 TCAACGCCAT CAGTGGGACT CCAACAAGCA CAATGGTTCA CGGGATGACC AGCTCGTCTT CGGTCGTGTG ATTACATCTC 4160
4161 ATGGCCCGTG TGTGGGGACT TGCTTTGTCA TTTGCAAACT CAGGATGCTT TCCAAAGCCA ATCACTGGGG AGACCGAGCA 4240
4241 CAGGGAGGAC CAAGGGGAAG GGGAGAGAAA GGAAATAAAG AACAACGTTA TTTCTTAACA GACTTTCTAT AGGAGTTGTA 4320
4321 AGAAGGTGCA CATATTTTTT TAAATCTCAC TGGCAATATT CAAAGTTTTC ATTGTGTCTT AACAAAGGTG TGGTAGACAC 4400
4401 TCTTGAGCTG GACTTAGATT TTATTCTTCC TTGCAGAGTA GTGTTAGAAT AGATGGCCTA CAGAAAAAAA AGGTTCTGGG 4480
4481 ATCTACATGG CAGGGAGGGC TGCACTGACA TTGATGCCTG GGGGACCTTT TGCCTCGACT CGTGCCGGAA ATCTGATCGT 4560
4561 AATCAGGGTA CAGAACTTAC TAGTTTTGTC TAGGAGTATG TTGTATGACT AGGATTTGTG CTATTATCTC ATTCAACAAC 4640
4641 ATAGAGCAAG AATAGTGAGC TAACTGAGCT AGACACTCAA TTAATCCGCT ACTGGCTTCA AGTCAGAACT TTGTCATTAA 4720
4721 TCATCGACTC CGGGACGGTC ATATATGTAT TACATTTCTA CATTTTTAAT ACTCACATGG GCTTATGCAT TAAGTTTAAT 4800
4801 TGTGATAAAT TTGTGCTGGT CCAGTATATG CAATACACTT TAATGGTTTA TTCTTGTCAT AAAAATGTGC AATATGGAGA 4880
                                                                                            4898
4881 TGTATACAAG TCTTTACT
        |  10      |  20      |  30      |  40      |  50      |  60      |  70      |  80
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FIG.10G

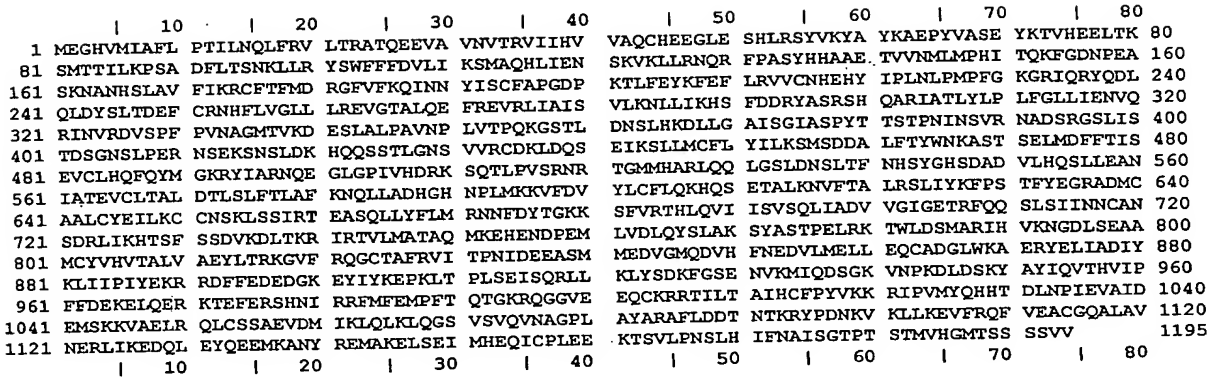
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80
1 MEGHVMIAFL PTILNQLFRV LTRATQEEVA VNVTRVIIHV VAQCHEEGLE SHLRSYVKYA YKAEPYVASE YKTVHEELTK 80
81 SMTTILKPSA DFLTSNKLLR YSWFFFDVLI KSMAQHLIEN SKVKLLRNQR FPASYHHAAE TVVNMLMPHI TQKFGDNPEA 160
161 SKNANHSLAV FIKRCFTFMD RGFVFKQINN YISCFAPGDP KTLFEYKFEF LRVVCNHEHY IPLNLPMPFG KGRIQRYQDL 240
241 QLDYSLTDEF CRNHFLVGLL LREVGTALQE FREVRLIAIS VLKNLLIKHS FDDRYASRSH QARIATLYLP LFGLLIENVQ 320
321 RINVRDVSPF PVNAGMTVKD ESLALPAVNP LVTPQKGSTL DNSLHKDLLG AISGIASPYT TSTPNINSVR NADSRGSLIS 400
401 TDSGNSLPER NSEKSNSLDK HQQSSTLGNS VVRCDKLDQS EIKSLLMCFL YILKSMSDDA LFTYWNKAST SELMDFFTIS 480
481 EVCLHQFQYM GKRYIARNQE GLGPIVHDRK SQTLPVSRNR TGMMHARLQQ LGSLDNSLTF NHSYGHSDAD VLHQSLLEAN 560
561 IATEVCLTAL DTLSLFTLAF KNQLLADHGH NPLMKKVFDV YLCFLQKHQS ETALKNVFTA LRSLIYKFPS TFYEGRADMC 640
641 AALCYEILKC CNSKLSSIRT EASQLLYFLM RNNFDYTGKK SFVRTHLQVI ISVSQLIADV VGIGETRFQQ SLSIINNCAN 720
721 SDRLIKHTSF SSDVKDLTKR IRTVLMATAQ MKEHENDPEM LVDLQYSLAK SYASTPELRK TWLDSMARIH VKNGDLSEAA 800
801 MCYVHVTALV AEYLTRKGVF RQGCTAFRVI TPNIDEEASM MEDVGMQDVH FNEDVLMELL EQCADGLWKA ERYELIADIY 880
881 KLIIPIYEKR RDFFEDEDGK EYIYKEPKLT PLSEISQRLL KLYSDKFGSE NVKMIQDSGK VNPKDLDSKY AYIQVTHVIP 960
961 FFDEKEILQER KTEFERSHNI RRFMFEMPFT QTGKRQGGVE EQCKRRTILT AIHCFPYVKK RIPVMYQHHT DLNPIEVAID 1040
1041 EMSKKVAELR QLCSSAEVDM IKLQLKLQGS VSVQVNAGPL AYARAFLDDT NTKRYPDNKV KLLKEVFRQF VEACGQALAV 1120
1121 NERLIKEDQL EYQEEMKANY REMAKELSEI MHEQICPLEE KTSVLPNSLH IFNAISGTPT STMVHGMTSS SSVV 1195
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80

FIG. 10G (cont.)

```
        |  10      |  20      |  30      |  40      |  50      |  60      |  70      |  80
  1 AATTGTAATA CGACTCACTA TAGGGCGAAT TGGGTACCGG  GCCCCCCCTC GAGGTCGACG GTATCGATAA GCTTGATATC 80
 81 GAATTCGGCA CGAGTTTTAC ACCATCACCA AAACCCAGAA  TTTTATGATG AGATTAAAAT AGAGTTGCCC ACTCAGCTGC 160
161 ATGAAAAGCA CCACCTGTTG CTCACATTCT TCCATGTCAG  CTGTGACAAC TCAAGTAAAG GAAGCACGAA GAAGAGGGAT 240
241 GTCGTTGAAA CCCAAGTTGG CTACTCCTGG CTTCCCCTCC  TGAAAGACGG AAGGGTGGTG ACAAGCGAGC AGCACATCCC 320
321 GGTCTCGGCG AACCTTCCTT CGGGCTATCT TGGCTACCAA  GAGCTTGGGA TGGGCAGGCA TTATGGTCCG GAAATTAAAT 400
401 GGGTAGATGG AGGCAAGCCA CTGCTGAAAA TTTCCACTCA  TCTGGTTTCT ACAGGGATAC TCAGGATCAG CATTTACATA 480
481 ATTTTTTCCA GTACTGTCAG AAAACCGAAT CTGGAGCCCA  AGCCTTAGGA AACGAACTTG TAAAGTACCT TAAGAGTCTG 560
561 CATGCGATGG AAGGCCACGT GATGATCGCC TTCTTGCCCA  CTATCCTAAA CCAGCTGTTC CGAGTCCTCA CCAGAGCCAC 640
641 ACAGGAAGAA GTCGCGGTTA ACGTGACTCG GGTCATTATT  CATGTGGTTG CCCAGTGCCA TGAGGAAGGA TTGGAGAGCC 720
721 ACTTGAGGTC ATATGTTAAG TACGCGTATA AGGCTGAGCC  ATATGTTGCC TCTGAATACA AGACAGTGCA TGAAGAACTG 800
801 ACCAAATCCA TGACCACGAT TCTCAAGCCT TCTGCCGATT  TCCTCACCAG CAACAAACTA CTGAGGTACT CATGGTTTTT 880
881 CTTTGATGTA CTGATCAAAT CTATGGCTCA GCATTTGATA  GAGAACTCCA AAGTTAAGTT GCTGCGAAAC CAGAGATTTC 960
961 CTGCATCCTA TCATCATGCA GCGGAAACCG TTGTAAATAT  GCTGATGCCA CACATCACTC AGAAGTTTGG AGATAATCCA 1040
1041 GAGGCATCTA AGAACGCGAA TCATAGCCTT GCTGTCTTCA  TCAAGAGATG TTTCACCTTC ATGGACAGGG GCTTTGTCTT 1120
1121 CAAGCAGATC AACAACTACA TTAGCTGTTT TGCTCCTGGA  GACCCAAAGA CCCTCTTTGA ATACAAGTTT GAATTTCTCC 1200
1201 GTGTAGTGTG CAACCATGAA CATTATATTC CGTTGAACTT  ACCAATGCCA TTTGGAAAAG GCAGGATTCA AAGATACCAA 1280
1281 GACCTCCAGC TTGACTACTC ATTAACAGAT GAGTTCTGCA  GAAACCACTT CTTGGTGGGA CTGTTACTGA GGGAGGTGGG 1360
1361 GACAGCCCTC CAGGAGTTCC GGGAGGTCCG TCTGATCGCC  ATCAGTGTGC TCAAGAACCT GCTGATAAAG CATTCTTTTG 1440
1441 ATGACAGATA TGCTTCAAGG AGCCATCAGG CAAGGATAGC  CACCCTCTAC CTGCCTCTGT TTGGTCTGCT GATTGAAAAC 1520
1521 GTCCAGCGGA TCAATGTGAG GGATGTGTCA CCCTTCCCTG  TGAACGCGGG CATGACCGTG AAGGATGAAT CCCTGGCTCT 1600
1601 ACCAGCTGTG AATCCGCTGG TGACGCCGCA GAAGGGAAGC  ACCCTGGACA ACAGCCTGCA CAAGGACCTG CTGGGCGCCA 1680
1681 TCTCCGGCAT TGCTTCTCCA TATACAACCT CAACTCCAAA  CATCAACAGT GTGAGAAATG CTGATTCGAG AGGATCTCTC 1760
1761 ATAAGCACAG ATTCGGGTAA CAGCCTTCCA GAAAGGAATA  GTGAGAAGAG CAATTCCCTG GATAAGCACC AACAAAGTAG 1840
1841 CACATTGGGA AATTCCGTGG TTCGCTGTGA TAAACTTGAC  CAGTCTGAGA TTAAGAGCCT ACTGATGTGT TTCCTCTACA 1920
1921 TCTTAAAGAG CATGTCTGAT GATGCTTTGT TTACATATTG  GAACAAGGCT TCAACATCTG AACTTATGGA TTTTTTTACA 2000
2001 ATATCTGAAG TCTGCCTGCA CCAGTTCCAG TACATGGGGA  AGCGATACAT AGCCAGGAAC CAGGAGGGGT TGGGACCCAT 2080
2081 AGTTCATGAT CGAAAGTCTC AGACATTGCC TGTTTCCCGT  AACAGAACAG GAATGATGCA TGCCAGATTG CAGCAGCTGG 2160
2161 GCAGCCTGGA TAACTCTCTC ACTTTTAACC ACAGCTATGG  CCACTCGGAC GCAGATGTTC TGCACCAGTC ATTACTTGAA 2240
2241 GCCAACATTG CTACTGAGGT TTGCCTGACA GCTCTGGACA  CGCTTTCTCT ATTTACATTG GCGTTTAAGA ACCAGCTCCT 2320
2321 GGCCGACCAT GGACATAATC CTCTCATGAA AAAAGTTTTT  GATGTCTACC TGTGTTTTCT TCAAAAACAT CAGTCTGAAA 2400
2401 CGGCTTTAAA AAATGTCTTC ACTGCCTTAA GGTCCTTAAT  TTATAAGTTT CCCTCAACAT TCTATGAAGG GAGAGCGGAC 2480
2481 ATGTGTGCGG CTCTGTGTTA CGAGATTCTC AAGTGCTGTA  ACTCCAAGCT GAGCTCCATC AGGACGGAGG CCTCCCAGCT 2560
2561 GCTCTACTTC CTGATGAGGA ACAACTTTGA TTACACTGGA  AAGAAGTCCT TTGTCCGGAC ACATTTGCAA GTCATCATAT 2640
2641 CTGTCAGCCA GCTGATAGCA GACGTTGTTG GCATTGGGGA  AACCAGATTC CAGCAGTCCC TGTCCATCAT CAACAACTGT 2720
2721 GCCAACAGTG ACCGGCTTAT TAAGCACACC AGCTTCTCCT  CTGATGTGAA GGACTTAACC AAAAGGATAC GCACGGTGCT 2800
2801 AATGGCCACC GCCCAGATGA AGGAGCATGA GAACGACCCA  GAGATGCTGG TGGACCTCCA GTACAGCCTG GCCAAATCCT 2880
2881 ATGCCAGCAC GCCCGAGCTC AGGAAGACGT GGCTCGACAG  CATGGCCAGG ATCCATGTCA AAAATGGCGA TCTCTCAGAG 2960
2961 GCAGCAATGT GCTATGTCCA CGTAACAGCC CTAGTGGCAG  AATATCTCAC ACGGAAAGGC GTGTTTAGAC AAGGATGCAC 3040
3041 CGCCTTCAGG GTCATTACCC CAAACATCGA CGAGGAGGCC  TCCATGATGG AAGACGTGGG GATGCAGGAT GTCCATTTCA 3120
3121 ACGAGGATGT GCTGATGGAG CTCCTTGAGC AGTGCGCAGA  TGGACTCTGG AAAGCCGAGC GCTACGAGCT CATCGCCGAC 3200
3201 ATCTACAAAC TTATCATCCC CATTTATGAG AAGCGGAGGG  ATTTCTTTGA AGATGAAGAT GGAAAGGAGT ATATTTACAA 3280
3281 GGAACCCAAA CTCACACCGC TGTCGGAAAT TTCTCAGAGA  CTCCTTAAAC TGTACTCGGA TAAATTTGGT TCTGAAAATG 3360
3361 TCAAAATGAT ACAGGATTCT GGCAAGGTCA ACCCTAAGGA  TCTGGATTCT AAGTATGCAT ACATCCAGGT GACTCACGTC 3440
3441 ATCCCCTTCT TTGACGAAAA AGAGTTGCAA GAAAGGAAAA  CAGAGTTTGA GAGATCCCAC AACATCCGCC GCTTCATGTT 3520
3521 TGAGATGCCA TTTACGCAGA CCGGGAAGAG GCAGGGCGGG  GTGGAAGAGC AGTGCAAACG GCGCACCATC CTGACAGCCA 3600
3601 TACACTGCTT CCCTTATGTG AAGAAGCGCA TCCCTGTCAT  GTACCAGCAC CACACTGACC TGAACCCCAT CGAGGTGGCC 3680
3681 ATTGACGAGA TGAGTAAGAA GGTGGCGGAG CTCCGGCAGC  TGTGCTCCTC GGCCGAGGTG GACATGATCA AACTGCAGCT 3760
3761 CAAACTCCAG GGCAGCGTGA GTGTTCAGGT CAATGCTGGC  CCACTAGCAT ATGCGCGAGC TTTCTTAGAT GATACAAACA 3840
3841 CAAAGCGATA TCCTGACAAT AAAGTGAAGC TGCTTAAGGA  AGTTTTCAGG CAATTTGTGG AAGCTTGCGG TCAAGCCTTA 3920
3921 GCGGTAAACG AACGTCTGAT TAAAGAAGAC CAGCTCGAGT  ATCAGGAAGA AATGAAAGCC AACTACAGGG AAATGGCGAA 4000
4001 GGAGCTTTCT GAAATCATGC ATGAGCAGAT CTGCCCCCTG  GAGGAGAAGA CGAGCGTCTT ACCGAATTCC CTTCACATCT 4080
4081 TCAACGCCAT CAGTGGGACT CCAACAAGCA CAATGGTTCA  CGGGATGACC AGCTCGTCTT CGGTCGTGTG ATTACATCTC 4160
4161 ATGGCCCGTG TGTGGGGACT TGCTTTGTCA TTTGCAAACT  CAGGATGCTT TCCAAAGCCA ATCACTGGGG AGACCGAGCA 4240
4241 CAGGGAGGAC CAAGGGGAAG GGGAGAGAAA GGAAATAAAG  AACAACGTTA TTTCTTAACA GACTTTCTAT AGGAGTTGTA 4320
4321 AGAAGGTGCA CATATTTTTT TAAATCTCAC TGGCAATATT  CAAAGTTTTC ATTGTGTCTT AACAAAGGTG TGGTAGACAC 4400
4401 TCTTGAGCTG GACTTAGATT TTATTCTTCC TTGCAGAGTA  GTGTTAGAAT AGATGGCCTA CAGAAAAAAA AGGTTCTGGG 4480
4481 ATCTACATGG CAGGGAGGGC TGCACTGACA TTGATGCCTG  GGGGACCTTT TGCCTCGACT CGTGCCGGAA ATCTGATCGT 4560
4561 AATCAGGGTA CAGAACTTAC TAGTTTTGTC TAGGAGTATG  TTGTATGACT AGGATTTGTG CTATTATCTC ATTCAACAAC 4640
4641 ATAGAGCAAG AATAGTGAGC TAACTGAGCT AGACACTCAA  TTAATCCGCT ACTGGCTTCA AGTCAGAACT TTGTCATTAA 4720
4721 TCATCGACTC CGGGACGGTC ATATATGTAT TACATTTCTA  CATTTTTAAT ACTCACATGG GCTTATGCAT TAAGTTTAAT 4800
4801 TGTGATAAAT TTGTGCTGGT CCAGTATATG CAATACACTT  TAATGGTTTA TTCTTGTCAT AAAAATGTGC AATATGGAGA 4880
4881 TGTATACAAG TCTTTACT                                                                    4898
        |  10      |  20      |  30      |  40      |  50      |  60      |  70      |  80
```

FIG.10H

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        |  10       |  20       |  30       |  40       |  50       |  60       |  70       |  80
  1 MEGHVMIAFL PTILNQLFRV LTRATQEEVA VNVTRVIIHV VAQCHEEGLE SHLRSYVKYA YKAEPYVASE YKTVHEELTK 80
 81 SMTTILKPSA DFLTSNKLLR YSWFFFDVLI KSMAQHLIEN SKVKLLRNQR FPASYHHAAE.TVVNMLMPHI TQKFGDNPEA 160
161 SKNANHSLAV FIKRCFTFMD RGFVFKQINN YISCFAPGDP KTLFEYKFEF LRVVCNHEHY IPLNLPMPFG KGRIQRYQDL 240
241 QLDYSLTDEF CRNHFLVGLL LREVGTALQE FREVRLIAIS VLKNLLIKHS FDDRYASRSH QARIATLYLP LFGLLIENVQ 320
321 RINVRDVSPF PVNAGMTVKD ESLALPAVNP LVTPQKGSTL DNSLHKDLLG AISGIASPYT TSTPNINSVR NADSRGSLIS 400
401 TDSGNSLPER NSEKSNSLDK HQQSSTLGNS VVRCDKLDQS EIKSLLMCFL YILKSMSDDA LFTYWNKAST SELMDFFTIS 480
481 EVCLHQFQYM GKRYIARNQE GLGPIVHDRK SQTLPVSRNR TGMMHARLQQ LGSLDNSLTF NHSYGHSDAD VLHQSLLEAN 560
561 IATEVCLTAL DTLSLFTLAF KNQLLADHGH NPLMKKVFDV YLCFLQKHQS ETALKNVFTA LRSLIYKFPS TFYEGRADMC 640
641 AALCYEILKC CNSKLSSIRT EASQLLYFLM RNNFDYTGKK SFVRTHLQVI ISVSQLIADV VGIGETRFQQ SLSIINNCAN 720
721 SDRLIKHTSF SSDVKDLTKR IRTVLMATAQ MKEHENDPEM LVDLQYSLAK SYASTPELRK TWLDSMARIH VKNGDLSEAA 800
801 MCYVHVTALV AEYLTRKGVF RQGCTAFRVI TPNIDEEASM MEDVGMQDVH FNEDVLMELL EQCADGLWKA ERYELIADIY 880
881 KLIIPIYEKR RDFFEDEDGK EYIYKEPKLT PLSEISQRLL KLYSDKFGSE NVKMIQDSGK VNPKDLDSKY AYIQVTHVIP 960
961 FFDEKEILQER KTEFERSHNI RRFMFEMPFT QTGKRQGGVE EQCKRRTILT AIHCFPYVKK RIPVMYQHHT DLNPIEVAID 1040
1041 EMSKKVAELR QLCSSAEVDM IKLQLKLQGS VSVQVNAGPL AYARAFLDDT NTKRYPDNKV KLLKEVFRQF VEACGQALAV 1120
1121 NERLIKEDQL EYQEEMKANY REMAKELSEI MHEQICPLEE KTSVLPNSLH IFNAISGTPT STMVHGMTSS SSVV      1195
        |  10       |  20       |  30       |  40       |  50       |  60       |  70       |  80
```

FIG. 10H (cont.)